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 Botstein, David
 Desnoyers, Luc
 Eaton, Dan L.
 Ferrara, Napoleone
 Fong, Sherman
 Gao, Wei-Qiang
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, Christopher J.
 Gurney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Smith, Victoria
 Stewart, Timothy A.
 Tumas, Daniel
 Watanabe, Colin K.
 Williams, P. Mickey
 Wood, William I.

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Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu
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Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val
				80					85					90

Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly
				95					100					105

Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala
				110					115					120

Pro	Thr	Asp	Trp	Leu	Thr	Leu	Glu	Asp	Tyr	Arg	Glu	Pro	Ile	Glu
				125					130					135

Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro
				140					145					150

Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val
				155					160					165

Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Gly	Tyr	Thr	Pro	Ser	Lys
				170					175					180

Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys
				185					190					195

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys	
				200					205					210	
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala	
				215					220					225	
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu	
				230					235					240	
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser	
				245					250					255	
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His	
				260					265					270	
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys	
				275					280					285	
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala	
				290					295					300	
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn	
				305					310					315	
Pro	Lys	Ala	Val												

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
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 gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200
 atgacaacag caagagtgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300
 gcttttctgt ggactcctct totacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggttaaaac cagcaaattc acccgtctta ccagctctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650

gagcgggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
agtgcacatg aactatcgcc agaagggcgt gattgacgtc ttcctgcatg 800
catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
gtgtccaggt ccttcagtga gtgggttggc ctcggtctca cactgatcga 900
cgcgctggac accatgtgga tcttggtctt gaggaagaa tttgaggaag 950
ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000
aacctgtttg agagcacgat ccgcatcctg ggggggctcc tgagtgccta 1050
ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100
atcggctaata gctgccttc agaacaccat ccaagattcc ttactcggat 1150
gtgaacatcg gtactggagt tgcccaccg ccacggtgga cctccgacag 1200
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cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350
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ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450
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ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
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 cagtcttgggt gtgatgcggg gtgggctggg cgcctggagc ctccgcctgc 2350
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 ctcagatgtc cccaatccaa gggctctggag gggctgccgt gactccagag 2550
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 ttgatttgct ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
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 1 5 10 15
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys		110	115	120
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val		125	130	135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro		140	145	150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro		155	160	165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly		170	175	180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro		185	190	195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly		200	205	210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg		215	220	225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln		230	235	240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp		245	250	255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly		260	265	270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe		275	280	285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile		290	295	300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser		305	310	315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu		320	325	330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu		335	340	345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn		350	355	360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser		365	370	375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr		380	385	390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe				

				395					400					405
Arg	Glu	Leu	Ser	Arg 410	Leu	Thr	Gly	Asp	Lys 415	Lys	Phe	Gln	Glu	Ala 420
Val	Glu	Lys	Val	Thr 425	Gln	His	Ile	His	Gly 430	Leu	Ser	Gly	Lys	Lys 435
Asp	Gly	Leu	Val	Pro 440	Met	Phe	Ile	Asn	Thr 445	His	Ser	Gly	Leu	Phe 450
Thr	His	Leu	Gly	Val 455	Phe	Thr	Leu	Gly	Ala 460	Arg	Ala	Asp	Ser	Tyr 465
Tyr	Glu	Tyr	Leu	Leu 470	Lys	Gln	Trp	Ile	Gln 475	Gly	Gly	Lys	Gln	Glu 480
Thr	Gln	Leu	Leu	Glu 485	Asp	Tyr	Val	Glu	Ala 490	Ile	Glu	Gly	Val	Arg 495
Thr	His	Leu	Leu	Arg 500	His	Ser	Glu	Pro	Ser 505	Lys	Leu	Thr	Phe	Val 510
Gly	Glu	Leu	Ala	His 515	Gly	Arg	Phe	Ser	Ala 520	Lys	Met	Asp	His	Leu 525
Val	Cys	Phe	Leu	Pro 530	Gly	Thr	Leu	Ala	Leu 535	Gly	Val	Tyr	His	Gly 540
Leu	Pro	Ala	Ser	His 545	Met	Glu	Leu	Ala	Gln 550	Glu	Leu	Met	Glu	Thr 555
Cys	Tyr	Gln	Met	Asn 560	Arg	Gln	Met	Glu	Thr 565	Gly	Leu	Ser	Pro	Glu 570
Ile	Val	His	Phe	Asn 575	Leu	Tyr	Pro	Gln	Pro 580	Gly	Arg	Arg	Asp	Val 585
Glu	Val	Lys	Pro	Ala 590	Asp	Arg	His	Asn	Leu 595	Leu	Arg	Pro	Glu	Thr 600
Val	Glu	Ser	Leu	Phe 605	Tyr	Leu	Tyr	Arg	Val 610	Thr	Gly	Asp	Arg	Lys 615
Tyr	Gln	Asp	Trp	Gly 620	Trp	Glu	Ile	Leu	Gln 625	Ser	Phe	Ser	Arg	Phe 630
Thr	Arg	Val	Pro	Ser 635	Gly	Gly	Tyr	Ser	Ser 640	Ile	Asn	Asn	Val	Gln 645
Asp	Pro	Gln	Lys	Pro 650	Glu	Pro	Arg	Asp	Lys 655	Met	Glu	Ser	Phe	Phe 660
Leu	Gly	Glu	Thr	Leu 665	Lys	Tyr	Leu	Phe	Leu 670	Leu	Phe	Ser	Asp	Asp 675
Pro	Asn	Leu	Leu	Ser 680	Leu	Asp	Ala	Tyr	Val 685	Phe	Asn	Thr	Glu	Ala 690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccggggccg gccgggctgc gagcgccctgc 50
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gcgagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tcaacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

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cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
cccaccgcct ggcaagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400
ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgtctc accaggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550
attgccatgc acgacgttga cctgtccct ctcaacgagg agctggacta 600
tggctttcct gaggtgtggc ccttcacgt ggcctccccg gagctccacc 650
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cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggtgtggg 750
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accatgtggc ttcccgact gccctgtctg tgggcggggc cccctgcact 1000
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cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450
tgaacaggac aacctotcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaa 1524

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<210> 17
<211> 327
<212> PRT
<213> Homo sapiens

<220>

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<221> sig_peptide
<222> 1-42
<223> Signal peptide.

<220>
<221> misc_feature
<222> 19-25,65-71,247-253,285-291,303-310
<223> N-myristoylation site.

<220>
<221> misc_feature
<222> 27-31
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
<221> TRANSMEM
<222> 29-49
<223> Transmembrane domain (type II).

<220>
<221> misc_feature
<222> 154-158
<223> N-glycosylation site.

<220>
<221> misc_feature
<222> 226-233
<223> Tyrosine kinase phosphorylation site.

<400> 17
Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1             5             10             15

Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
          20             25             30

Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
          35             40             45

Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
          50             55             60

Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
          65             70             75

Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
          80             85             90

Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
          95             100            105

Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
          110            115            120

Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
          125            130            135

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

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				140					145					150
Glu	Ser	Ser	Asn	Ser 155	Thr	Asp	Tyr	Ile	Ala 160	Met	His	Asp	Val	Asp 165
Leu	Leu	Pro	Leu	Asn 170	Glu	Glu	Leu	Asp	Tyr 175	Gly	Phe	Pro	Glu	Ala 180
Gly	Pro	Phe	His	Val 185	Ala	Ser	Pro	Glu	Leu 190	His	Pro	Leu	Tyr	His 195
Tyr	Lys	Thr	Tyr	Val 200	Gly	Gly	Ile	Leu	Leu 205	Leu	Ser	Lys	Gln	His 210
Tyr	Arg	Leu	Cys	Asn 215	Gly	Met	Ser	Asn	Arg 220	Phe	Trp	Gly	Trp	Gly 225
Arg	Glu	Asp	Asp	Glu 230	Phe	Tyr	Arg	Arg	Ile 235	Lys	Gly	Ala	Gly	Leu 240
Gln	Leu	Phe	Arg	Pro 245	Ser	Gly	Ile	Thr	Thr 250	Gly	Tyr	Lys	Thr	Phe 255
Arg	His	Leu	His	Asp 260	Pro	Ala	Trp	Arg	Lys 265	Arg	Asp	Gln	Lys	Arg 270
Ile	Ala	Ala	Gln	Lys 275	Gln	Glu	Gln	Phe	Lys 280	Val	Asp	Arg	Glu	Gly 285
Gly	Leu	Asn	Thr	Val 290	Lys	Tyr	His	Val	Ala 295	Ser	Arg	Thr	Ala	Leu 300
Ser	Val	Gly	Gly	Ala 305	Pro	Cys	Thr	Val	Leu 310	Asn	Ile	Met	Leu	Asp 315
Cys	Asp	Lys	Thr	Ala 320	Thr	Pro	Trp	Cys	Thr 325	Phe	Ser			

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<210> 18
<211> 23
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.
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<400> 18
gcgaacgctt cqaggaqtcc tqg 23
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<210> 19
<211> 24
<212> DNA
<213> Artificial
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<220>
<221> Artificial Sequence

<222> 1-24
 <223> Synthetic construct

<400> 19
 gcagtgcggg aagccacatg gtac 24

<210> 20
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 20
 cttctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
 <211> 494
 <212> DNA
 <213> Homo sapiens

<400> 21
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 aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
 gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
 gattgggcct tctttccccc ttcttttctg tgtctcctgc ctcatcggcc 200
 tgccatgacc tgcagccaag ccagagcccg tggggaaggg gagaaagtgg 250
 gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300
 ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
 atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
 cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
 taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-15
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccg 150
ggctccgggg cggcccgtga ggccagtgcg ccgcgcgtcg ccccgagggc 200
cccgccccgc agcatggagc caccggagc cggcgggggc cgcgcgcagc 250
cgccgctgtt gctgccgtc tcgctgttag cgctgctgc gctgctggga 300
ggcggcgggc gcggcgggc cgcggcgtg ccgcgggct gcaagcacga 350
tgggcgggcc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400
tggtgtgcag cagcctggaa ctgcgcagg tcctgcccc agatactctg 450
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccagct 500
gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
tctctaaaaa gattggtatc gacaaacaat cgaataggat gtctgaatgc 650
agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggga 700
atttgttttc ttcattatct caaggaactt ttgattatct tgogtcatta 750
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctgggtaa aggagaagaa catcacggtg cgggatacca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900
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Asp	Pro	Gly	Ala	Phe 125	Trp	Gly	Leu	Ser	Ser 130	Leu	Lys	Arg	Leu	Asp 135
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Gly	Leu	Thr	Asn	Leu 155	Val	Arg	Leu	Asn	Leu 160	Ser	Gly	Asn	Leu	Phe 165
Ser	Ser	Leu	Ser	Gln 170	Gly	Thr	Phe	Asp	Tyr 175	Leu	Ala	Ser	Leu	Arg 180
Ser	Leu	Glu	Phe	Gln 185	Thr	Glu	Tyr	Leu	Leu 190	Cys	Asp	Cys	Asn	Ile 195
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Asp	Thr	Arg	Cys	Val 215	Tyr	Pro	Lys	Ser	Leu 220	Gln	Ala	Gln	Pro	Val 225
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Ala	Gly	Ser	Thr	Gly 320	Asn	Trp	Gly	Cys	His 325	Val	Gln	Thr	Lys	Arg 330
Gly	Asn	Asn	Thr	Arg 335	Thr	Val	Asp	Ile	Val 340	Val	Leu	Glu	Ser	Ser 345
Ala	Gln	Tyr	Cys	Pro 350	Pro	Glu	Arg	Val	Val 355	Asn	Asn	Lys	Gly	Asp 360
Phe	Arg	Trp	Pro	Arg 365	Thr	Leu	Ala	Gly	Ile 370	Thr	Ala	Tyr	Leu	Gln 375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro

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Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly	Phe		
	395	400	405		
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp	Val		
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Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu	Thr		
	425	430	435		
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val	Glu		
	440	445	450		
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala	Glu		
	455	460	465		
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser	Lys		
	470	475	480		
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met	Leu		
	485	490	495		
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys	Ala		
	500	505	510		
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr	Arg		
	515	520	525		
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn	Ile		
	530	535	540		
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly	Met		
	545	550	555		
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr	Gly		
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Leu Ser Asp Tyr	Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp	Lys		
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Gln Leu Ser Phe	Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser	Leu		
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 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24

<223> Synthetic construct

<400> 25

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<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

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<212> DNA

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<223> Synthetic construct.

<400> 27

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

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cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250

atgacttgaa tgtgaaatat ctgttgagca gacaacacga gtttgtgtgt 300

gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350

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ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450

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tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

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gtggaggagg agacgctcct gatcgctcga tcc 683

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<211> 81
<212> PRT
<213> Homo sapiens

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<223> Signal peptide.

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35 40 45
Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
50 55 60
Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
65 70 75
Lys Gly Ser Gln Lys Ser
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<211> 2128
<212> DNA
<213> Homo sapiens

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<210> 31

<211> 322

<212> PRT

<213> Homo sapiens

<400> 31

Met	Pro	Val	Thr	Val	Thr	Arg	Thr	Thr	Ile	Thr	Thr	Thr	Thr	Thr	1	5	10	15
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Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val	35	40	45	
Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	50	55	60	
Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	65	70	75	
Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu	80	85	90	
Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	95	100	105	
Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr	110	115	120	
Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp	125	130	135	
His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala	140	145	150	
Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile	155	160	165	
Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu	170	175	180	
Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn	185	190	195	
Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Glu	Trp	Cys	Val	Ala	Val	Tyr	200	205	210	

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<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135

Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150

Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
				185					190					195

His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210

Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225

Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
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Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
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<210> 34

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct

<400> 34

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<210> 35

<211> 50

<212> DNA

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<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 40
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ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150
tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250
caatctattc ttgccacatc aagggattgt tattccttta aaaaaaacc 300

aataccaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350
caacgttggt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
taaacctatt tctttggaaa gtgaagcaaa cttaaaactca gataaagaaa 500
atataaccac ctcaaatctc aaggcgagtc attccctcc tttgaatcta 550
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gcattctttg ggcagtctaa aaccacatc taccatttc acaagccctc 650
ccttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700
gatgaagatc ttttgccat ctacgcacat cccaatgcta cacctgctct 750
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agcctacctt aaaattcacc aataattcaa aactctttcc aaatacgtca 1000
gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050
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cctccacttc gtacttctgt atagaactaa cagcaaaaag gcgttaaaca 1350
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ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450
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acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900
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aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000
aaggttttgg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050
ttgggtgcct taaaaactca atgagaatca tgggt 2084

<210> 41

<211> 334

<212> PRT

<213> Homo sapiens

<400> 41

Met	Leu	Ala	Leu	Ala	Lys	Ile	Leu	Leu	Ile	Ser	Thr	Leu	Phe	Tyr	1	5	10	15
Ser	Leu	Leu	Ser	Gly	Ser	His	Gly	Lys	Glu	Asn	Gln	Asp	Ile	Asn	20	25	30	
Thr	Thr	Gln	Asn	Ile	Ala	Glu	Val	Phe	Lys	Thr	Met	Glu	Asn	Lys	35	40	45	
Pro	Ile	Ser	Leu	Glu	Ser	Glu	Ala	Asn	Leu	Asn	Ser	Asp	Lys	Glu	50	55	60	
Asn	Ile	Thr	Thr	Ser	Asn	Leu	Lys	Ala	Ser	His	Ser	Pro	Pro	Leu	65	70	75	
Asn	Leu	Pro	Asn	Asn	Ser	His	Gly	Ile	Thr	Asp	Phe	Ser	Ser	Asn	80	85	90	
Ser	Ser	Ala	Glu	His	Ser	Leu	Gly	Ser	Leu	Lys	Pro	Thr	Ser	Thr	95	100	105	
Ile	Ser	Thr	Ser	Pro	Pro	Leu	Ile	His	Ser	Phe	Val	Ser	Lys	Val	110	115	120	
Pro	Trp	Asn	Ala	Pro	Ile	Ala	Asp	Glu	Asp	Leu	Leu	Pro	Ile	Ser	125	130	135	
Ala	His	Pro	Asn	Ala	Thr	Pro	Ala	Leu	Ser	Ser	Glu	Asn	Phe	Thr	140	145	150	
Trp	Ser	Leu	Val	Asn	Asp	Thr	Val	Lys	Thr	Pro	Asp	Asn	Ser	Ser	155	160	165	
Ile	Thr	Val	Ser	Ile	Leu	Ser	Ser	Glu	Pro	Thr	Ser	Pro	Ser	Val	170	175	180	
Thr	Pro	Leu	Ile	Val	Glu	Pro	Ser	Gly	Trp	Leu	Thr	Thr	Asn	Ser	185	190	195	

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
305 310 315

Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu
320 325 330

Arg Thr Ser Val

<210> 42
<211> 1594
<212> DNA
<213> Homo sapiens

<400> 42
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cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
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tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350
ttttgattct gaggatcctg caaattccct tcgtggagga gaggcctaact 400
tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
atcattgatg tgctgtccc cagtttctct gatagtgacc ctgcagcaat 500
tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgcc ctcaatactt ctattgttat gcctccaaaa 600
aatctggtag agctcttttg caaactggcg agtggcagat atctgcctca 650
aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700
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cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttggttgt 1200
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aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500
tgtgtaggtg ctgaatgctg taaggagttt aggttgtagt aattctacaa 1550
ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
				20					25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
				35					40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	50		55		60
Ser Phe Ile Leu	Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr			
	65	70			75
Lys Tyr Phe Met	Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys			
	80	85			90
Phe Phe Asp Ser	Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu			
	95	100			105
Pro Asn Phe Leu	Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp			
	110	115			120
Asp Asn Ile Ala	Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp			
	125	130			135
Ser Asp Pro Ala	Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr			
	140	145			150
Ala Tyr Leu Asp	Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu			
	155	160			165
Asn Thr Ser Ile	Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe			
	170	175			180
Gly Lys Leu Ala	Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val			
	185	190			195
Arg Glu Asp Leu	Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn			
	200	205			210
Leu Gly Ile Phe	Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe			
	215	220			225
Arg Leu Arg Arg	Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala			
	230	235			240
Ile Asp Lys Cys	Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile			
	245	250			255
Val Glu Thr Lys	Ile Cys Gln Glu				
	260				

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

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 gtttcggcgg cagcccccag cctcctcatc cttctgttgc tgctgctggg 200
 gtctgtgcct gctaccgacg cccgctctgt gccoctgaag gccacgttcc 250
 tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300
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 gccccagccc acaaccctg ggggcccata accccacc aacttcctgg 400
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 ggctccctgg cttttctgct gatgttcata gtctgtgccg cggtcatac 500
 ccggcagaag cagaaggcct cggcctatta cccatcgctc ttccccaaga 550
 agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600
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 cccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750
 ggcaggggcg cagaggaaga ggagaaggcg agccaggagg gggaccagga 800
 agtccaggga catgggggtcc cagtggagac accagaggcg caggaggagc 850
 cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900
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 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300
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 caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850
 gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg 950
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 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050
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 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacaggg 1250
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 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcac 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52

<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

Met	Lys	Phe	Gln	Gly	Pro	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Leu	Cys
1				5					10					15

Leu	Gly	Ser	Gly	Glu	Ala	Gly	Pro	Leu	Gln	Ser	Gly	Glu	Glu	Ser
				20					25					30

Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
				35					40					45

Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr					
				65					70					75					
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly					
				80					85					90					
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala					
				95					100					105					
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val					
				110					115					120					
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val					
				125					130					135					
Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile					
				140					145					150					
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro					
				155					160					165					
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser					
				170					175					180					
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln					
				185					190					195					
Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly					
				200					205					210					
Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln					
				215					220					225					
Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly					
				230					235					240					
Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser					
				245					250					255					
Gly	Ser	Gly	Ser	Asn	Gly	Asp	Asn	Asn	Asn	Gly	Ser	Ser	Ser	Gly					
				260					265					270					
Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser					
				275					280					285					
Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Gly	Asn	Ser	Gly	Gly	Ser					
				290					295					300					
Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly					
				305					310					315					
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His					
				320					325					330					
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly					
				335					340					345					

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
350 355 360
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
365 370 375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
380 385 390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
395 400 405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
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Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
425 430 435
Ser Ser Arg Ile Pro
440

<210> 53
<211> 3580
<212> DNA
<213> Homo sapiens

<400> 53
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ctttgctgac catgttggtc ccttgctgga atattaccgg gacatcttca 150
ctctcctgct gcgcctgcac cggagcttgg tgttgctgca ggagagtgag 200
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ttgcaacaga	gaaagcctgt	gcttggctgt	cagccaacat	cacagcactg	950
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gagttagctt	ccctcctcgt	tgcagatcaa	attcctatcc	tagggccccc	1250
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agccgagccc	cacctgccag	aaccccagct	aagagcctgt	gagttggtgc	1600
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<210> 54
<211> 280
<212> PRT
<213> Homo sapiens
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<400> 54

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Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
				155					160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
				185					190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
				200					205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245					250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
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<210> 55
 <211> 2401
 <212> DNA
 <213> Homo sapiens

<400> 55
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<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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Phe	Ala	Leu	Ile	Thr	Ile	Leu	Ile	Leu	Tyr	Ser	Ser	Asn	Ser	Ala
				20					25					30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg		35	40	45
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro		50	55	60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val		65	70	75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro		80	85	90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro		95	100	105
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg		110	115	120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly		140	145	150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val		155	160	165
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala		170	175	180
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly		185	190	195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val		215	220	225
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro		230	235	240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr			290	295	

<210> 57
 <211> 4277
 <212> DNA
 <213> Homo sapiens

<400> 57

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<210> 58
<211> 1115

<212> PRT
 <213> Homo sapiens

<400> 58

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				20					25					30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
				35					40					45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
				50					55					60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
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Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
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Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
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Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu	Leu
	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys	Met
	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu	Tyr
	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu	Ser
	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys	Glu
	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn	Ala
	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg	Ala
	365	370	375
Leu Arg Val Leu	Ser Met Gly Pro Glu	Asp Glu Gly Val Tyr	Gln
	380	385	390
Cys Met Ala Glu	Asn Glu Val Gly Ser	Ala His Ala Val Val	Gln
	395	400	405
Leu Arg Thr Ser	Arg Pro Ser Ile Thr	Pro Arg Leu Trp Gln	Asp
	410	415	420
Ala Glu Leu Ala	Thr Gly Thr Pro Pro	Val Ser Pro Ser Lys	Leu
	425	430	435
Gly Asn Pro Glu	Gln Met Leu Arg Gly	Gln Pro Ala Leu Pro	Arg
	440	445	450
Pro Pro Thr Ser	Val Gly Pro Ala Ser	Pro Lys Cys Pro Gly	Glu
	455	460	465
Lys Gly Gln Gly	Ala Pro Ala Glu Ala	Pro Ile Ile Leu Ser	Ser
	470	475	480
Pro Arg Thr Ser	Lys Thr Asp Ser Tyr	Glu Leu Val Trp Arg	Pro
	485	490	495
Arg His Glu Gly	Ser Gly Arg Ala Pro	Ile Leu Tyr Tyr Val	Val
	500	505	510
Lys His Arg Lys	Gln Val Thr Asn Ser	Ser Asp Asp Trp Thr	Ile
	515	520	525
Ser Gly Ile Pro	Ala Asn Gln His Arg	Leu Thr Leu Thr Arg	Leu
	530	535	540
Asp Pro Gly Ser	Leu Tyr Glu Val Glu	Met Ala Ala Tyr Asn	Cys
	545	550	555
Ala Gly Glu Gly	Gln Thr Ala Met Val	Thr Phe Arg Thr Gly	Arg

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Arg Pro Lys Pro	Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile	Gln		
	575		580		585
Arg Asp Asp Pro	Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro	Asp		
	590		595		600
His Gly Arg Leu	Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr	Ile		
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Ser Thr Ala Ser	Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro	Arg		
	620		625		630
Gly Asn Gly Gly	Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr	Lys		
	635		640		645
Lys Leu Lys Lys	Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala	Ile		
	650		655		660
Pro Pro Ser Arg	Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys	Gly		
	665		670		675
Thr Ser Tyr Lys	Phe Arg Val Arg Ala	Leu Asn Met Leu Gly	Glu		
	680		685		690
Ser Glu Pro Ser	Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly	Tyr		
	695		700		705
Ser Gly Arg Val	Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile	Thr		
	710		715		720
Phe Thr Asp Ala	Val Asn Glu Thr Thr	Ile Met Leu Lys Trp	Met		
	725		730		735
Tyr Ile Pro Ala	Ser Asn Asn Asn Thr	Pro Ile His Gly Phe	Tyr		
	740		745		750
Ile Tyr Tyr Arg	Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr	Lys		
	755		760		765
Lys Asp Met Val	Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser	His		
	770		775		780
Leu Gln Pro Glu	Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe	Asn		
	785		790		795
Glu Gly Gly Glu	Ser Glu Phe Ser Asn	Val Met Ile Cys Glu	Thr		
	800		805		810
Lys Ala Arg Lys	Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro	Pro		
	815		820		825
Thr Leu Ala Pro	Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu	Arg		
	830		835		840
Pro Val Gly Thr	Gly Ala Met Val Ala	Arg Ser Ser Asp Leu	Pro		
	845		850		855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
860 865 870

Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
875 880 885

Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
890 895 900

Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
905 910 915

Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
920 925 930

Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
935 940 945

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
950 955 960

Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
965 970 975

Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
980 985 990

Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
995 1000 1005

Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
1010 1015 1020

Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
1025 1030 1035

Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
1040 1045 1050

Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
1055 1060 1065

Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
1070 1075 1080

Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
1085 1090 1095

Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
1100 1105 1110

Pro Pro Leu Thr Ile
1115

<210> 59
<211> 25
<212> DNA
<213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 59
 gggaaacaca gcagtcattg cctgc 25

<210> 60
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 60
 gcacacgtag cctgtcgctg gaggc 24

<210> 61
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 61
 caccacaaag ccaggtccg gtacagcgctc aaacaagagt gg 42

<210> 62
 <211> 1661
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 678
 <223> unknown base

<400> 62
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 cgcctgtctc tcccaggctc ccgcgccga ccccgcgca acatgcagcc 100
 cacgggcccgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgctc 150
 tgctgtctcct gctactgctg ctgtctgtgc ggcagcccgt aaccgcgcgc 200
 gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250
 cctcttcacc acgcccgggtg tcccagcgc cctcactacc ccaggcctca 300
 ctacgccagg caccacaaa accctggacc ttcggggctc gcgcaggcc 350

ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
tcagccatgg tcagaccagc ctggacagggc ttagagacgg cctcgtgggt 500
gccagttctt ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600
cctactctga actcgagctt gtgacctcag ctgaaggctt gaacagctct 650
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cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800
agacaccaca tgtacaccaa cgtcagcggg ttgacaagct ttggtgagaa 850
agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
catcggacac cttgataaga agggctcctg aagtgtctca ggctcctgtg 950
atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000
tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatggtga 1050
cactgtccat ggggggtgctg cagtgcgaacc tgcttgctaa cgtgtccact 1100
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cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350
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tgctgacaca gtcgggtccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
cacatggaaa a 1661

<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	1	5	10	15
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	20	25	30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

	260		265		270
Ser Asp Thr Leu	Ile Arg Arg Val Leu	Glu Val Ser Gln Ala Pro			
	275	280			285
Val Ile Phe Ser	His Ser Ala Ala Arg	Ala Val Cys Asp Asn Leu			
	290	295			300
Leu Asn Val Pro	Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly Gly			
	305	310			315
Ile Val Met Val	Thr Leu Ser Met Gly	Val Leu Gln Cys Asn Leu			
	320	325			330
Leu Ala Asn Val	Ser Thr Val Ala Asp	His Phe Asp His Ile Arg			
	335	340			345
Ala Val Ile Gly	Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp			
	350	355			360
Gly Thr Gly Arg	Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr			
	365	370			375
Pro Val Leu Ile	Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu			
	380	385			390
Glu Leu Gln Gly	Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg			
	395	400			405
Gln Val Glu Lys	Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val			
	410	415			420
Glu Ala Glu Phe	Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser			
	425	430			435
His Leu Val Pro	Gln Asn Gly His Gln	Ala Thr His Leu Glu Val			
	440	445			450
Thr Lys Gln Pro	Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala			
	455	460			465
Ser Pro Tyr Leu	Val Pro Gly Leu Val	Ala Ala Ala Thr Ile Pro			
	470	475			480
Thr Phe Thr Gln	Trp Leu Cys				
	485				

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacaccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
ggcccagcaa gcttgataag catgaagctc ttatctttgg tggctgtggt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650
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ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
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ctccttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850
aagagggatg tgggtctctga tctctgttgt cttcttgggt ctttgggggt 900
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cagctctgag tcttgggaat gttgttacc cttggaagata aagctgggtc 1050
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gcctcttgtc cctgaaactc gttgtaccag tgcattggaga gaaaattttg 1500
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ttttatttct ctca 1564

<210> 68
<211> 183
<212> PRT
<213> Homo sapiens

<400> 68
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
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Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
20 25 30
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
35 40 45
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
65 70 75
Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
80 85 90
Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
95 100 105
Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
110 115 120
Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
125 130 135
Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
140 145 150
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
155 160 165
Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180
Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
agcgggtctc gcttggttc cgtaatttc tgtcctgagg cgtgagactg 50
agttcatagg gtctgggtc cccgaaccag gaagggttga gggaaacaaa 100
tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggtcctccc 150
tccctttgca ttccacccc tccgggcttt gcgctttcct ggggaccccc 200
tcgccgggag atggccgctg tgatgcggag caaggattcg tcctgctgcc 250
tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
tcgcgggcca aactcaactc catcaagtcc tctctgggag gggagacgcc 350
tggtcaggcc gccaatgat ctgcgggcat gtaccaagga ctggcattcg 400
gcggcagtaa gaaggcaaa aacctggggc aggcctaccc ttgtagcagt 450
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atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550
gcatgtgctg cccagtagc cgtgcaata atggcatctg tatccagtt 600
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cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700
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gaccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800
tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850
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gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150
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agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300
aagagtttag gttgtgctgg aggagagggt tccttcagat tgctgattgc 1350
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aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaatt 1450
gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500
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cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650
ccacaaatac ttttttttca aaattttagt ttacctgta attaataaga 1700
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agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050
aaaacttttt cgtttggtca ggttttggca acacatagat catatgtctg 2100

aggcacaagt	tggctgttca	tctttgaaac	caggggatgc	acagtctaaa	2150
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tcagtgtgag	gtcctgtgtc	cgtactatcc	tcaaattatt	tattttatag	2250
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tcttgaagta	gacagagtag	tgagggttca	ttgccctcta	taagcttctg	2350
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aaatataagt	aggataactt	gtaaaacctg	catattgcta	atctatagac	2500
accacagttt	ctaaattctt	tgaaaccact	ttactacttt	ttttaaactt	2550
aactcagttc	taaatacttt	gtctggagca	caaaacaata	aaaggttatc	2600
ttatagtcgt	gaotttaaac	ttttgtagac	cacaattcac	tttttagttt	2650
tcttttactt	aaatcccato	tgcagttctc	aatttaagtt	ctcccagtag	2700
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tatttactaa	gatgattaag	acttacattt	tctgcacagg	tctgcaaaaa	2800
caaaaaattat	aaactagtcc	atccaagaac	caaagtttgt	ataaacagggt	2850
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atataacaat	tattatattt	acaatttggt	ttctgcaata	tttttcttat	2950
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ttaatgagat	gtattttctt	atagagatat	ttcttacaga	aagctttgta	3050
gcagaatata	tttgcagcta	ttgactttgt	aatttaggaa	aaatgtataa	3100
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aaaaaaaaaa	aaaaaaaaaa	3170			

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
20 25 30

Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
50 55 60

Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
65 70 75

Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
80 85 90

His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
95 100 105

Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
125 130 135

Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
140 145 150

Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
155 160 165

Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
170 175 180

Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
185 190 195

Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
200 205 210

Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
215 220 225

Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
230 235 240

Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
245 250 255

Cys Gln Lys Ile

<210> 71
<211> 1809
<212> DNA
<213> Homo sapiens

<400> 71
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tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccggcca 100
acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
cttccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250
 atatttttagt aattcatatg ttttagatta taggttttaa cataacttgtg 300
 aaaataacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
 ggatttgttc ttttatcccc cttttaaaagt catccgtcct tggctcagga 400
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 tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
 gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
 ctcaagcccc caacatccca gtccctcagtc ctccagtcac ttgacttcaa 600
 atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650
 agcaccagag ccaggcagtc actgttcctc ctccctgggtt ggagtccttt 700
 ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750
 tgtgaacaag cttttgcagc ttcccagcac gaccattgaa aatatctctg 800
 tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
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 agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttgggt 950
 cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaaaatagt 1000
 aatcagattc ccatcagctt gtattcgaag tctttaagtg agcctttgaa 1050
 tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100
 ccgtcattac ctccctgcag ctgacaagct catcactgaa ttctgctagt 1150
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 gatagctcac gtgatgtgga aaacaccagt tggatcaatg ctcatctgtt 1400
 aaaaagcagc ccttttgcct ttttgttttt ggaccagggtg ttggctgtgg 1450
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 ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550
 tttaaagatg cttgggccag gcgggggtggc tgatgcccac aatcccagtg 1600
 ctttgggggg ccaaggcagg cagattgcc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
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ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
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20 25 30
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360
Leu	Ile	Arg												

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
 aattcatggc aaatattttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
 tggtaaaactg gcccaaactc gg 22

<210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac cgcgccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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cgcgaccgcg tggctgtggg cgcggatgcc tttgagcgcg gtgacttctc 500
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ccactctcag caccacacat ttgcatctgc tgggtggacct gccaccatca 1950
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30
Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75

Ala Arg Gly Ala	Pro	Ala Leu Leu Thr	Cys	Val Asn Arg Gly	His
	80		85		90
Val Trp Thr Asp	Arg	His Val Glu Glu	Ala Gln Gln Val	Val	His
	95		100		105
Trp Asp Arg Gln	Pro	Pro Gly Val Pro	His Asp Arg Ala	Asp Arg	
	110		115		120
Leu Leu Asp Leu	Tyr	Ala Ser Gly Glu	Arg Arg Ala Tyr	Gly Pro	
	125		130		135
Leu Phe Leu Arg	Asp	Arg Val Ala Val	Gly Ala Asp Ala	Phe Glu	
	140		145		150
Arg Gly Asp Phe	Ser	Leu Arg Ile Glu	Pro Leu Glu Val	Ala Asp	
	155		160		165
Glu Gly Thr Tyr	Ser	Cys His Leu His	His His Tyr Cys	Gly Leu	
	170		175		180
His Glu Arg Arg	Val	Phe His Leu Thr	Val Ala Glu Pro	His Ala	
	185		190		195
Glu Pro Pro Pro	Arg	Gly Ser Pro Gly	Asn Gly Ser Ser	His Ser	
	200		205		210
Gly Ala Pro Gly	Pro	Asp Pro Thr Leu	Ala Arg Gly His	Asn Val	
	215		220		225
Ile Asn Val Ile	Val	Pro Glu Ser Arg	Ala His Phe Phe	Gln Gln	
	230		235		240
Leu Gly Tyr Val	Leu	Ala Thr Leu Leu	Leu Phe Ile Leu	Leu Leu	
	245		250		255
Val Thr Val Leu	Leu	Ala Ala Arg Arg	Arg Arg Gly Gly	Tyr Glu	
	260		265		270
Tyr Ser Asp Gln	Lys	Ser Gly Lys Ser	Lys Gly Lys Asp	Val Asn	
	275		280		285
Leu Ala Glu Phe	Ala	Val Ala Ala Gly	Asp Gln Met Leu	Tyr Arg	
	290		295		300
Ser Glu Asp Ile	Gln	Leu Asp Tyr Lys	Asn Asn Ile Leu	Lys Glu	
	305		310		315
Arg Ala Glu Leu	Ala	His Ser Pro Leu	Pro Ala Lys Tyr	Ile Asp	
	320		325		330
Leu Asp Lys Gly	Phe	Arg Lys Glu Asn	Cys Lys		
	335		340		

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200
atcttcttca gcttgggcat tggcagtcta ctgccatgga acttctttat 250
cactgccaag gagtactgga tgttcaaact cgcgaactcc tccagcccag 300
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gccattggtt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79
<211> 475
<212> PRT
<213> Homo sapiens

<400> 79
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
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Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
20 25 30
Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75
Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

	395		400		405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser			
	410	415		420	
Leu Leu Gly Leu	Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu Leu			
	425	430		435	
Tyr Gly Pro Lys	Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr Gly			
	440	445		450	
Val Val Met Ser	Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly Ser			
	455	460		465	
Ala Cys Ser Thr	Leu Leu Val His Leu	Ile			
	470	475			

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu
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Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln
				20					25					30
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu
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Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln
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Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala
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Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala
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Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn
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Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser
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His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu
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Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His
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Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys
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Leu Gly Tyr Ala	Leu Arg Pro Gln Glu	Lys Gly His Ser Pro	Glu
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Asp Ile Tyr Gln	Met Ala Leu Asn Gln	Ala Leu Lys Asp Leu	Lys
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Ala Leu Gly Cys	Arg Lys Ala Met Lys	Lys Phe Glu Arg His	Thr
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Leu Leu Glu Tyr	Leu Leu Gly Glu Gly	Asn Leu Ser Arg Pro	Ala
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Val Gln Leu Leu	Gly Asp Val Met Ser	Glu Asp Gly Phe Phe	Tyr
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Arg Leu Gln Tyr	Ser Arg Ile Val Gly	Gly Trp Asp Leu Leu	Pro
260		265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn	Ala
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Pro Val Val Ala	Met Thr Gln Gly Pro	His Asp Val His Val	Gln
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Ile Glu Thr Ser	Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys	Ala
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Asp Val Val Leu	Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg	Ile
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Thr Phe Ser Pro	Pro Leu Pro Arg His	Met Gln Glu Ala Leu	Arg
335		340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys	Val Phe Leu Ser Phe	Arg
350		355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile	Glu Gly Gly His Ser	Asn
365		370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg	Glu
380		385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala	Ala
395		400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala	Leu
410		415	420
Asp Asp Val Ala	Ala Leu His Gly Pro	Val Val Arg Gln Leu	Trp
425		430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp	Ala Glu Asp Gln His	Ser
440		445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro	Ala Leu Trp Gln Thr	Glu

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Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys		
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Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro		
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Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu		
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<212> DNA
<213> Homo sapiens
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<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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			20					25						30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	35	40	45
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	140	145	150
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Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	185	190	195
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Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	290	295	300
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Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr			

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His	Gln	Asn	Ile	Val 335	Ser	Asn	Ala	Ala	Ala	Phe	Leu	Lys	Cys	Val 345
Glu	His	Ala	Tyr	Glu 350	Pro	Thr	Pro	Asp	Asp	Val	Ala	Ile	Ser	Tyr 360
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Tyr	Ser	Cys	Gly	Ala 380	Arg	Val	Gly	Phe	Phe	Gln	Gly	Asp	Ile	Arg 390
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Ala	Val	Pro	Arg	Leu 410	Leu	Asn	Arg	Ile	Tyr	Asp	Lys	Val	Gln	Asn 420
Glu	Ala	Lys	Thr	Pro 425	Leu	Lys	Lys	Phe	Leu	Leu	Lys	Leu	Ala	Val 435
Ser	Ser	Lys	Phe	Lys 440	Glu	Leu	Gln	Lys	Gly	Ile	Ile	Arg	His	Asp 450
Ser	Phe	Trp	Asp	Lys 455	Leu	Ile	Phe	Ala	Lys	Ile	Gln	Asp	Ser	Leu 465
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Ala	Cys	Asn	Tyr	Val 530	Lys	Leu	Glu	Asp	Val	Ala	Asp	Met	Asn	Tyr 540
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Leu	Asp	Ser	Asp	Gly 575	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Arg	Trp 585
Leu	Pro	Asn	Gly	Thr 590	Leu	Lys	Ile	Ile	Asp	Arg	Lys	Lys	Asn	Ile 600
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Thr Tyr Ser Pro His Glu Asp Glu Ala Met	Val Leu Phe Leu Asn	155	160	165
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Gly Ser Phe His Leu Lys Asp Thr Ala Lys	Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly	Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val	Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly	Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu	Glu Ala Glu Cys His	245	250	255
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Lys Val Glu Gly Tyr Gly Ser Val Cys Ser	Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro	Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn	Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala	Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr	Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly	Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln	His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu	Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val	Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu	Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr	Glu His Thr Ala Glu			

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Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
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Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
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Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
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Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
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<213> Artificial

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<222> 1-22
<223> Synthetic construct.

<400> 90
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<210> 91
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<222> 1-47
<223> Synthetic construct.

<400> 93
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<210> 94
<211> 3037
<212> DNA
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<400> 94

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe	Ser Ala Gly Thr Phe Leu	
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro	Glu Val Gly Gly Ile Gly	
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser Arg	
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu Ile	
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 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 96
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<210> 97
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<220>
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 <223> Synthetic construct.

<400> 97
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<220>
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<210> 99
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<212> DNA

<213> Homo sapiens

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
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Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
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Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
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Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
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Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
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Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
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Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
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Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
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Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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Glu	Val	Val	Leu	Asp	Ser	Lys	Arg	Gln	Val	Glu	Lys	Glu	Glu	Thr	245	250	255
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Pro	Gln	Glu	Pro	Gly	Arg	Glu	Gln	Val	Val	Glu	Asp	Arg	Pro	Val	275	280	285
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Gln	Val	Gln	Ala	Ala	Leu	Ser	Val	Ser	Gln	Glu	Asn	Pro	Glu	Met	305	310	315
Glu	Gly	Pro	Glu	Arg	Asp	Gln	Leu	Val	Ile	Pro	Asp	Gly	Gln	Glu	320	325	330
Glu	Glu	Gln	Glu	Ala	Ala	Gly	Glu	Gly	Arg	Asn	Gln	Gln	Lys	Leu	335	340	345
Arg	Gly	Glu	Asp	Asp	Tyr	Asn	Met	Asp	Glu	Asn	Glu	Ala	Glu	Ser	350	355	360
Glu	Thr	Asp	Lys	Gln	Ala	Ala	Leu	Ala	Gly	Asn	Asp	Arg	Asn	Ile	365	370	375
Asp	Val	Phe	Asn	Val	Glu	Asp	Gln	Lys	Arg	Asp	Thr	Ile	Asn	Leu	380	385	390
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<210> 101

<211> 3671

<212> DNA

<213> Homo sapiens

<400> 101

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<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	170	175	180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	185	190	195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly				

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Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys			
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His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met			
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Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr			
				260					265					270			
Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp			
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His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu			
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Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro			
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Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu			
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Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile			
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Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	
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Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	
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Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	
				695					700					705	
Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	
				710					715					720	
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	
				725					730					735	
Val	Ser	Gly	Ala	Ser	Met	Val	Leu	Pro	Arg	Ala	Val	Ala	Gly	Leu	
				740					745					750	
Ala	Ala	Ser	Gly	Leu	Ala	Leu	Leu	Leu	Trp	Lys	Pro	Val	Thr	Val	
				755					760					765	
Leu	Val	Lys	Ala	Gly	Ala	Gly	Ala	Pro	Arg	Thr	Arg	Thr	Val	Leu	
				770					775					780	
Thr	Pro	Phe	Ser	Gly	Pro	Pro	Thr	Ser	Gln	Ala	Asp	Leu	Asp	Tyr	

	785		790		795
Val Val Pro Gln Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly	800		805		810
Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala	815		820		825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu	830		835		840
Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile	845		850		855
Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu	860		865		870
His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe	875		880		885
Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr	890		895		900
Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile	905		910		915
His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser	920		925		930
Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala	935		940		945
Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp	950		955		960
Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro	965		970		975
Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu	980		985		990
Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe	995		1000		1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu	1010		1015		1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg	1025		1030		1035
Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe	1040		1045		1050
Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly	1055		1060		1065
Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe	1070		1075		1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

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<211> 1743
<212> DNA
<213> Homo sapiens

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ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtcatt tctgttgtcc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatacaac agaactgtgt cccagtgtgt gaccaaccac acgctgggtg 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
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aagacttaga cccctggcg caggagcaca cagactcgga ggagggggcg 1200
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Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	
				170					175					180	
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	
				185					190					195	
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	
				200					205					210	
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	
				215					220					225	
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	
				230					235					240	
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	
				245					250					255	
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	
				260					265					270	
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	
				275					280					285	
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	
				290					295					300	
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	
				305					310					315	
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	
				320					325					330	
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	
				335					340					345	
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	
				350					355					360	
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	
				365					370					375	
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	
				380					385					390	
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	
				395					400					405	
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	
				410					415					420	
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	
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<210> 105

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<211> 21
<212> DNA
<213> Artificial

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<222> 1-21
<223> Synthetic construct

<400> 105
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<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
    cagtgtgccca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
    agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct.

<400> 108
    ctctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

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<222> 1-51
<223> Synthetic construct.

<400> 109
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c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
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cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgctgact gtggccaccg cctgatgct gcccgtaag cccccgcag 150
gctcctgggg ggcccagatc atcgggggcc acgaggtgac ccccaactcc 200
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
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acagagacct ccgcaactggc ctggtggtgc tgggcgcca cgtcctgagt 350
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aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

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				20					25					30

Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
			35						40					45

Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60

Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75

Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90

His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105

Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120

Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135

Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150

Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165

Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180

Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195

Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210

Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225

Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240

Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
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Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
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<210> 112
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 112
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<210> 113
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-44
 <223> Synthetic construct.

<400> 114
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<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

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Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
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Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
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Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

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Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	245	250	255
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	260	265	270
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	275	280	285
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	290	295	300
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	305	310	315
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	320	325	330
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	335	340	345
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	350	355	360
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	365	370	375
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	380	385	390
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	395	400	405
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	410	415	420
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	425	430	435
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	440	445	450
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	455	460	465
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	470	475	480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	485	490	495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	500	505	510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	515	520	525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser			

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

cgggacagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

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gaatcggccc tggcaggtgg ggccaagagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
 gtcttattct tgccottccc ccaaccagtt tgттаатcaa асаатааааа 1750
 catgttttgt tttgttttta аааааааа 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
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 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230		235		240
Ile Leu Leu Pro Gln Phe Leu Gly Val	245	Leu Leu Thr Leu Leu Tyr	250		255
Ile Thr Arg Val Glu Asp Ile Ile Met	260	Glu His Ser Val Thr Asp	265		270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	275	Ser Val Glu Ala Ala Gly	280		285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn	290				

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
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<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
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<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

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ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
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gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtcaa 450
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ccattcagct ctacctgggg gccaaagttgt tggactcaca gggaaagggtg 850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcagcctca tcgtgagtca ggacgtggtg aaagctgcag 950
tggctgctgt gctctctcca gaagaattca tggctcctgtt ggactctgtg 1000
cttcctgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050
aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc 1100
aggacactcc cgagtttttt atagaccaag gccatgcca ggtggcccaa 1150
ctgatcgtgc tggaagtgtt tcctccagt gaagccctcc gccctttgtt 1200
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accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctggggg cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450

Ser Ile Asp Arg	Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile Lys	230	235	240
Gly Asp Thr Ile	Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp Ser	245	250	255
Gln Gly Lys Val	Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser Leu	260	265	270
Thr Met Pro Thr	Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val Ser	275	280	285
Gln Asp Val Val	Lys Ala Ala Val Ala	Ala Val Leu Ser Pro Glu	290	295	300
Glu Phe Met Val	Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala His	305	310	315
Arg Leu Lys Ser	Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala Asp	320	325	330
Lys Leu Gly Ser	Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp Thr	335	340	345
Pro Glu Phe Phe	Ile Asp Gln Gly His	Ala Lys Val Ala Gln Leu	350	355	360
Ile Val Leu Glu	Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro Leu	365	370	375
Phe Thr Leu Gly	Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr Thr	380	385	390
Lys Gly Asp Gln	Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser Asp	395	400	405
Arg Ile Gln Leu	Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro Asp	410	415	420
Val Leu Lys Asn	Ile Ile Thr Glu Ile	Ile His Ser Ile Leu Leu	425	430	435
Pro Asn Gln Asn	Gly Lys Leu Arg Ser	Gly Val Pro Val Ser Leu	440	445	450
Val Lys Ala Leu	Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr Lys	455	460	465
Asp Ala Leu Val	Leu Thr Pro Ala Ser	Leu Trp Lys Pro Ser Ser	470	475	480
Pro Val Ser Gln					

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

[illegible]

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Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	
				125					130					135	
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	
				140					145					150	
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	
				155					160					165	
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	
				170					175					180	
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	
				185					190					195	
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	
				200					205					210	
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	
				215					220					225	
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	
				230					235					240	
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	
				245					250					255	
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	
				260					265					270	
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	
				275					280					285	
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	
				290					295					300	
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	
				305					310					315	
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	
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Ser	Phe	Leu	Met	Ser											
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<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

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 cttggcgctg gcggtactgg ccccgaggc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
 aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
 ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
 atggatggat gtcattggaga ggcatggcta ccgaacacag aaatttgga 500
 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
 tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggg 600
 taatcttctc cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
 agaatacaga caaagcagta aactgggtta gaaaggaagc aattaattac 700
 actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750
 ttcaccatct tctggagaaa attttgatc ttcaacattt cacacatctc 800
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 tcacctttgt cagaaatgca ccctgtagat tattactctt cttatacaaa 900
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aatcacatat tttcaaaaat ggttattatt taggcctttg tacaatttct 2250
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atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450
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<210> 132
<211> 536
<212> PRT
<213> Homo sapiens

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20 25 30
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
35 40 45
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
50 55 60
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
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Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
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Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
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Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

				365					370					375
Leu	Ser	Gly	Tyr	Ser 380	Leu	Leu	Pro	Leu	Ser 385	Ser	Glu	Thr	Phe	Lys 390
Asn	Glu	His	Lys	Val 395	Lys	Asn	Leu	His	Pro 400	Pro	Trp	Ile	Leu	Ser 405
Glu	Phe	His	Gly	Cys 410	Asn	Val	Asn	Ala	Ser 415	Thr	Tyr	Met	Leu	Arg 420
Thr	Asn	His	Trp	Lys 425	Tyr	Ile	Ala	Tyr	Ser 430	Asp	Gly	Ala	Ser	Ile 435
Leu	Pro	Gln	Leu	Phe 440	Asp	Leu	Ser	Ser	Asp 445	Pro	Asp	Glu	Leu	Thr 450
Asn	Val	Ala	Val	Lys 455	Phe	Pro	Glu	Ile	Thr 460	Tyr	Ser	Leu	Asp	Gln 465
Lys	Leu	His	Ser	Ile 470	Ile	Asn	Tyr	Pro	Lys 475	Val	Ser	Ala	Ser	Val 480
His	Gln	Tyr	Asn	Lys 485	Glu	Gln	Phe	Ile	Lys 490	Trp	Lys	Gln	Ser	Ile 495
Gly	Gln	Asn	Tyr	Ser 500	Asn	Val	Ile	Ala	Asn 505	Leu	Arg	Trp	His	Gln 510
Asp	Trp	Gln	Lys	Glu 515	Pro	Arg	Lys	Tyr	Glu 520	Asn	Ala	Ile	Asp	Gln 525
Trp	Leu	Lys	Thr	His 530	Met	Asn	Pro	Arg	Ala 535	Val				

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<210> 133
<211> 1475
<212> DNA
<213> Homo sapiens
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<400> 133					
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gcttctactg	agaggtctgc	catggcctct	cttggcctcc	aacttggtggg	150
ctacatccta	ggccttctgg	ggcttttggg	cacactgggt	gccatgctgc	200
tccccagctg	gaaaacaagt	tcttatgtcg	gtgccagcat	tgtgacagca	250
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tccaggctgc	ccaggccatg	atggtgacat	ccagtgcaat	ctcctccctg	400
gcctgcatta	tctctgtggt	gggcatgaga	tgcacaagtct	tctgccagga	450

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<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu
1				5					10				15	

Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
				20					25				30	

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
				35					40				45	

Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Ile Thr Gln Cys Asp 65	Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala 70 75	
Asp Ile Gln Ala Ala 80	Gln Ala Met Met Val Thr Ser Ser Ala Ile 85 90	
Ser Ser Leu Ala Cys 95	Ile Ile Ser Val Val Gly Met Arg Cys Thr 100 105	
Val Phe Cys Gln Glu 110	Ser Arg Ala Lys Asp Arg Val Ala Val Ala 115 120	
Gly Gly Val Phe Phe 125	Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro 130 135	
Val Ala Trp Asn Leu 140	His Gly Ile Leu Arg Asp Phe Tyr Ser Pro 145 150	
Leu Val Pro Asp Ser 155	Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr 160 165	
Leu Gly Ile Ile Ser 170	Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile 175 180	
Leu Cys Phe Ser Cys 185	Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr 190 195	
Asp Ala Tyr Gln Ala 200	Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg 205 210	
Pro Gly Gln Pro Pro 215	Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser 220 225	
Leu Thr Gly Tyr Val 230		

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
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 aagtcacgcg tcccgctggc tcagaacctat ggctgtgcca gccggcaccc 150
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cgccatcgtg tccctgagcg agaccgcca atgtggtccc cctgcacct 250
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 gattttgttg tgaagctgaa gggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
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<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
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 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys
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Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
			20					25						30
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35					40						45
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50					55						60
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65					70						75
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80					85						90
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95					100						105
Cys	Arg	Ser	Val	Ser										
			110											

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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	140		145		150
Ile Arg His His	His Ser Glu His Arg Val His Gly Ala Met Glu				
	155		160		165
Leu Gln Val Gln	Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val				
	170		175		180
Tyr Pro Ser Ser	Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala				
	185		190		195
Leu Ala Thr Gly	Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu				
	200		205		210
Ile Leu Leu Leu	Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg				
	215		220		225
Arg Ala Gln Glu	Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile				
	230		235		240
Glu Asn Pro Gly	Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro				
	245		250		255
Glu Ala Lys Val	Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln				
	260		265		270
Pro Ser Glu Ser	Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro				
	275		280		285
Leu Ser Pro Pro	Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp				
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Pro Val Pro Asp	Ser Pro Asn Phe Glu Val Ile				
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<210> 141

<211> 1732

<212> DNA

<213> Homo sapiens

<400> 141

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<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	1	5	10	15
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	20	25	30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	110	115	120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys				

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450
Thr		

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
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 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
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 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
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<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750
 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225

Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
260 265 270

Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
275 280 285

Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
290 295 300

Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
305 310 315

Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
320 325 330

Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
335 340 345

Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
350 355 360

Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
365 370 375

Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
380 385 390

Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
395 400 405

Val

<210> 147

<211> 2052

<212> DNA

<213> Homo sapiens

<400> 147

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catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200

ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgttttg 250

gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300

gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350

agggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400

gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450

attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
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cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900
ccacctctca ggtgaagaac cgtcaggaat tccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
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aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	1	5	10	15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	20	25	30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	35	40	45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	50	55	60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	65	70	75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	80	85	90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	95	100	105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	110	115	120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	125	130	135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	140	145	150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	155	160	165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	170	175	180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	185	190	195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	200	205	210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	215	220	225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu				

230					235					240				
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe	Gly	Ile	Val	Gly	Leu	Lys
				245										255
Ile	Phe	Phe	Ser	Lys	Phe	Gln	Trp	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260										270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275										285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290										300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305										315
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
				320										330
Val	Ala	Ser	Gln	Ser	Phe	Gln	Ala	Gly	Lys	His	Tyr	Trp	Glu	Val
				335										345
Asp	Gly	Gly	His	Asn	Lys	Arg	Trp	Arg	Val	Gly	Val	Cys	Arg	Asp
				350										360
Asp	Val	Asp	Arg	Arg	Lys	Glu	Tyr	Val	Thr	Leu	Ser	Pro	Asp	His
				365										375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Asn	Gly	Glu	His	Leu	Tyr	Phe	Thr
				380										390
Leu	Asn	Pro	Arg	Phe	Ile	Ser	Val	Phe	Pro	Arg	Thr	Pro	Pro	Thr
				395										405
Lys	Ile	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Cys	Gly	Thr	Ile	Ser	Phe
				410										420
Phe	Asn	Ile	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Thr	Cys	Arg
				425										435
Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Glu	Tyr	Pro	Ser	Tyr	Asn
				440										450
Glu	Gln	Asn	Gly	Thr	Pro	Ile	Val	Ile	Cys	Pro	Val	Thr	Gln	Glu
				455										465
Ser	Glu	Lys	Glu	Ala	Ser	Trp	Gln	Arg	Ala	Ser	Ala	Ile	Pro	Glu
				470										480
Thr	Ser	Asn	Ser	Glu	Ser	Ser	Ser	Gln	Ala	Thr	Thr	Pro	Phe	Leu
				485										495
Pro	Arg	Gly	Glu	Met										
				500										

<210> 149

<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggettcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgccg ccgccgcgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cgttggcggc ggggccgcgg ggcaggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggc cccgcgcgc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

cacccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcggccc ctcgccgacc acccctccgg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550
tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
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tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
agaccacagg gcagtgtgag tgctcgccag gttatcaggg gcttcactgt 800
gaaacctgca aagagggttt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
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gggtcataga ttacaaaaat attttatata cttttattct cttactttat 1050
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agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
1 5 10 15

Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
20 25 30

Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
35 40 45

Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
50 55 60

Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
65 70 75

Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
80 85 90

Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
95 100 105

Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
110 115 120

Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
125 130 135

Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
140 145 150

Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
155 160 165

Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
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 ttctggcttt ggtctcgggtg cccagggccc aggccgtgtg gttgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
 ccgggaaaag ggctttgccg tggagaagga catgaagaac gtctgtgggg 200
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
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 ttctggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttctgtgc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
 gggctctgtg acctcggcca gtgtccaccc acctcgtca gcggctcccg 650
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95						100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
			110						115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
			125						130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
			140						145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
			155						160					

<210> 159
 <211> 1665
 <212> DNA
 <213> Homo sapiens

<400> 159
 aacagacgtt cctcgcggc cctggcacct ctaaccccag acatgctgct 50
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 gtaaaactgct gacgatgcag agttccgtga cggcgcagga aggcctgtgt 150
 gtccatgtgc cctgctcctt ctccacccc tcgcatggct ggatttaccc 200
 tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
 aggatgctcc agtggccaca aacaaccag ctccggcagt gtgggaggag 300
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tccagggcac 500
 cctggagtcc ggctgcccc agaactctgac ctgctctgtg ccctgggcct 550
 gtgagcaggg gacaccccct atgatctcct ggataggac ctccgtgtcc 600
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 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
 tggctctgtc agttgatgca gttgacagca atccccctgc caggctgagc 900
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ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
 gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050
 ctgcagagca aagccacatc aggagtgact caggggggtgg tcggggggagc 1100
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 tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcagggggcc 1250
 cctgactgaa ccttggggcag aagacagtcc cccagaccag cctccccag 1300
 cttctgccccg ctctctcagt ggggaaggag agctccagta tgcattccctc 1350
 agcttccaga tgggtgaagcc ttgggactcg cggggacagg aggccactga 1400
 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500
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 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160
 <211> 463
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala
 1 5 10 15
 Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
 20 25 30
 Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
 35 40 45
 Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
 50 55 60
 Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
 65 70 75
 Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
 80 85 90
 Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
 95 100 105
 Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

				110					115					120	
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	
				125					130					135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	
				140					145					150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	
				155					160					165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	
				170					175					180	
Ile	Gly	Thr	Ser	Val	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Thr	Arg	Ser	
				185					190					195	
Ser	Val	Leu	Thr	Leu	Ile	Pro	Gln	Pro	Gln	Asp	His	Gly	Thr	Ser	
				200					205					210	
Leu	Thr	Cys	Gln	Val	Thr	Phe	Pro	Gly	Ala	Ser	Val	Thr	Thr	Asn	
				215					220					225	
Lys	Thr	Val	His	Leu	Asn	Val	Ser	Tyr	Pro	Pro	Gln	Asn	Leu	Thr	
				230					235					240	
Met	Thr	Val	Phe	Gln	Gly	Asp	Gly	Thr	Val	Ser	Thr	Val	Leu	Gly	
				245					250					255	
Asn	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Glu	Gly	Gln	Ser	Leu	Arg	Leu	
				260					265					270	
Val	Cys	Ala	Val	Asp	Ala	Val	Asp	Ser	Asn	Pro	Pro	Ala	Arg	Leu	
				275					280					285	
Ser	Leu	Ser	Trp	Arg	Gly	Leu	Thr	Leu	Cys	Pro	Ser	Gln	Pro	Ser	
				290					295					300	
Asn	Pro	Gly	Val	Leu	Glu	Leu	Pro	Trp	Val	His	Leu	Arg	Asp	Ala	
				305					310					315	
Ala	Glu	Phe	Thr	Cys	Arg	Ala	Gln	Asn	Pro	Leu	Gly	Ser	Gln	Gln	
				320					325					330	
Val	Tyr	Leu	Asn	Val	Ser	Leu	Gln	Ser	Lys	Ala	Thr	Ser	Gly	Val	
				335					340					345	
Thr	Gln	Gly	Val	Val	Gly	Gly	Ala	Gly	Ala	Thr	Ala	Leu	Val	Phe	
				350					355					360	
Leu	Ser	Phe	Cys	Val	Ile	Phe	Val	Val	Val	Arg	Ser	Cys	Arg	Lys	
				365					370					375	
Lys	Ser	Ala	Arg	Pro	Ala	Ala	Gly	Val	Gly	Asp	Thr	Gly	Ile	Glu	
				380					385					390	
Asp	Ala	Asn	Ala	Val	Arg	Gly	Ser	Ala	Ser	Gln	Gly	Pro	Leu	Thr	
				395					400					405	

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcca ggagggacca ctacatcttt tactgcaaag accagacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccg 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacce tccagccatg acccttcct 650
 gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

[illegible]

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<210> 163
<211> 22
<212> DNA
<213> Artificial
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```
<220>  
<221> Artificial Sequence  
<222> 1-22  
<223> Synthetic construct.
```

```
<400> 163
ggagatgaag accctgttcc tg 22
```

```
<210> 164
<211> 26
<212> DNA
<213> Artificial
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```
<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.
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```
<400> 164
ggagatgaag accctgttcc tgggtg 26
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<210> 165
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct.

<400> 165
 gtcctccgga aagtccttat c 21

<210> 166
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 166
 gcctagtgtt cgggaacgca gcttc 25

<210> 167
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 167
 cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 168
 ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169
 <211> 1204
 <212> DNA
 <213> Homo sapiens

<400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtgggg 250
cgacgtcat cgccccaga tggctcctga cagcagcca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccgacag cactgagtc cttccccac ccgggttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcaccctctc 500
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gcacgtccag ccccgagta cgctgcctc acaccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
attatctcct ggggccagga tccgtgtgcg atcaccogaa agcctggtgt 800
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acaattagac tggaccacc caccacagcc catcacctc catttccact 900
tggtgtttgg ttcctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100
tgtatcccca gcccacaaag cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro		20	25	30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu		35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala		50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His		65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr		80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys		95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val		110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys		125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr		140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn		155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly		170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly		185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn		200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala		215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val		230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn							245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171
ggctgcggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc gggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggcctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattotactg cagccggaca 250

caaaatgaag gccaccccaa atggtttggtt cttgggtgttg ggcaagtcatt 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 181
 gtgttctgct ggagccgatg cc 22

<210> 182
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 182
 gacatggaca atgacagg 18

<210> 183
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 183
 cctttcagga tgtaggag 18

<210> 184
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcatcctgat atgacttgtc acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggctg aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgcttggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500
gcccctgccc aatgactgtg caaccgctgg caccgagtgc caggtctcag 550
gctggggcat caccaaccac ccacggaacc cattcccgga tctgctccag 600
tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
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atgcctgcca gggtgattct gggggcccc tgggtgtgtg gggagtctt 750
caaggtcttg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
 ccctagctcc actcttgttg gcctgggaac ttcttggaac tttaactcct 1000
 gccagccctt ctaagaccca cgagcggggt gagagaagtg tgcaatagtc 1050
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

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Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
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 ctcgctccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga agaagatgat ctgagagggtg acaggagggg 400
 tcagtgcacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg acccgcctg gactccccag ccttcccacc ccatacctcc 600
 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
 tttgtttggt cattgagggt ttgtttgtgt tttcatcaat gtctttgtaa 700
 agcaciaaatt atctgcctta aaggggctct gggtcgggga atoctgagcc 750
 ttgggtcccc tcctctctct cttccctcct tcccgcctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcaggagg 850
 cttccagcct gtgttccct cacttgaggg aaccagcact ctccatcctt 900
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950
 gacccaggc cactctgaga agaccttgga gtagggacaa ggctgcaggg 1000
 cctctttcgg gtttccttgg acagtgccat ggttccagtg ctctggtgtc 1050

accaggaca cagccactcg gggccccgct gcccagctg atccccactc 1100
 attccacacc ttttctcatc ctcagtgatg tgaaggtggg aaggaaagga 1150
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300
 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450
 tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe
1				5					10					15

Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
			20						25					30

Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
			35						40					45

Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
			50						55					60

Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
			65						70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
			80						85					90

Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
			95						100					105

Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
			110						115					120

Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
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<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

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				20				25						30
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val
				35				40						45
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro
				50				55						60
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg
				65				70						75
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu
				80				85						90
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe
				95				100						105
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys
				110				115						120
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu
				125				130						135
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg
				140				145						150
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp
				155				160						165

Asn Asn His Ile	Ser Cys Ile Glu Asp	Gly Ala Phe Arg Ala	Leu
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Arg Asp Leu Glu	Ile Leu Thr Leu Asn	Asn Asn Asn Ile Ser	Arg
185		190	195
Ile Leu Val Thr	Ser Phe Asn His Met	Pro Lys Ile Arg Thr	Leu
200		205	210
Arg Leu His Ser	Asn His Leu Tyr Cys	Asp Cys His Leu Ala	Trp
215		220	225
Leu Ser Asp Trp	Leu Arg Gln Arg Arg	Thr Val Gly Gln Phe	Thr
230		235	240
Leu Cys Met Ala	Pro Val His Leu Arg	Gly Phe Asn Val Ala	Asp
245		250	255
Val Gln Lys Lys	Glu Tyr Val Cys Pro	Ala Pro His Ser Glu	Pro
260		265	270
Pro Ser Cys Asn	Ala Asn Ser Ile Ser	Cys Pro Ser Pro Cys	Thr
275		280	285
Cys Ser Asn Asn	Ile Val Asp Cys Arg	Gly Lys Gly Leu Met	Glu
290		295	300
Ile Pro Ala Asn	Leu Pro Glu Gly Ile	Val Glu Ile Arg Leu	Glu
305		310	315
Gln Asn Ser Ile	Lys Ala Ile Pro Ala	Gly Ala Phe Thr Gln	Tyr
320		325	330
Lys Lys Leu Lys	Arg Ile Asp Ile Ser	Lys Asn Gln Ile Ser	Asp
335		340	345
Ile Ala Pro Asp	Ala Phe Gln Gly Leu	Lys Ser Leu Thr Ser	Leu
350		355	360
Val Leu Tyr Gly	Asn Lys Ile Thr Glu	Ile Ala Lys Gly Leu	Phe
365		370	375
Asp Gly Leu Val	Ser Leu Gln Leu Leu	Leu Leu Asn Ala Asn	Lys
380		385	390
Ile Asn Cys Leu	Arg Val Asn Thr Phe	Gln Asp Leu Gln Asn	Leu
395		400	405
Asn Leu Leu Ser	Leu Tyr Asp Asn Lys	Leu Gln Thr Ile Ser	Lys
410		415	420
Gly Leu Phe Ala	Pro Leu Gln Ser Ile	Gln Thr Leu His Leu	Ala
425		430	435
Gln Asn Pro Phe	Val Cys Asp Cys His	Leu Lys Trp Leu Ala	Asp
440		445	450
Tyr Leu Gln Asp	Asn Pro Ile Glu Thr	Ser Gly Ala Arg Cys	Ser

				455					460					465
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser
				470					475					480
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe
				485					490					495
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg
				500					505					510
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg
				515					520					525
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn
				530					535					540
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys
				545					550					555
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys
				560					565					570
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu
				575					580					585
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val
				590					595					600
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn
				605					610					615
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser
				620					625					630
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr
				635					640					645
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu
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Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly
				665					670					675
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys
				680					685					690
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala
				695					700					705
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln
				710					715					720
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val
				725					730					735
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met
				740					745					750

Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr	
				755					760						765
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile	
				770					775						780
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe	
				785					790						795
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg	
				800					805						810
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu	
				815					820						825
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu	
				830					835						840
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly	
				845					850						855
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu	
				860					865						870
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser	
				875					880						885
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr	
				890					895						900
His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala	
				905					910						915
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr	
				920					925						930
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr	
				935					940						945
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile	
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Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser	
				965					970						975
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly	
				980					985						990
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys	
				995					1000						1005
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys	
				1010					1015						1020
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile	
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Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys	

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Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
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Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
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His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
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His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
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Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
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Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
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Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
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Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
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Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
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Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
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Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
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Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
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1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
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Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
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Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
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Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
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Glu Cys Gly Cys Leu Ala Cys Ser
1520

<210> 199
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 199
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<210> 200
<211> 24
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttgcatc tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
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<222> 1-50
<223> Synthetic construct.

<400> 201
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<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

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gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
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gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
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 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattt gcatcccact gtccttgtgt tcggagccag gccacaccgt 50
cctcagcagt gtcattgtgt aaaaacgcca agctgaatat atcatgcccc 100
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250

agagagattc	ttttcttaaa	cgactataca	gggcccgaat	tgactggata	300
gaggaataca	ccacaggcat	ggcagactgc	atcttagtca	acagccagtt	350
cacagctgct	gtttttaagg	aaacattcaa	gtccctgtct	cacatagacc	400
ctgatgtcct	ctatccatct	ctaaatgtca	ccagctttga	ctcagttggt	450
cctgaaaagc	tggatgacct	agtccccaag	gggaaaaaat	tcctgctgct	500
ctccatcaac	agatacgaaa	ggaagaaaaa	tctgactttg	gcactggaag	550
ccctagtaca	gctgcgtgga	agattgacat	cccaagattg	ggagaggggt	600
catctgatcg	tggcagggtg	ttatgacgag	agagtcctgg	agaatgtgga	650
acattatcag	gaattgaaga	aaatggtcca	acagtccgac	cttggccagt	700
atgtgacctt	cttgagggtct	ttctcagaca	aacagaaaat	ctccctcctc	750
cacagctgca	cgtgtgtgct	ttacacacca	agcaatgagc	actttggcat	800
tgccctctg	gaagccatgt	acatgcagtg	ccagtcatt	gctgttaatt	850
cgggtggacc	cttggagttc	attgaccaca	gtgtcacagg	gtttctgtgt	900
gagcctgacc	cggtgcactt	ctcagaagca	atagaaaagt	tcatccgtga	950
accttcctta	aaagccacca	tgggcctggc	tggaagagcc	agagtgaagg	1000
aaaaattttc	ccctgaagca	tttacagaac	agctctaccg	atatgttacc	1050
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ttatggattg	tagaccagtg	tttgaaacca	aaaaagaaac	ctagaatcta	1150
atgcagaaga	gatcttttta	aaaataaaact	tgagtcttga	atgtgagcca	1200
ctttcctata	taccacacct	ccctgtccac	ttttcagaaa	aaccatgtct	1250
tttatgctat	aatcattcca	aattttgcca	gtgttaagtt	acaaatgtgg	1300
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tgctcttctg	tctataaatt	ttgaatgata	ctgtgcctta	attggttttc	1400
atagtttaag	tgtgtatcat	tatcaaagtt	gattaatttg	gottcatagt	1450
ataatgagag	cagggctatt	gtagttccca	gattcaatcc	accgaagtgt	1500
tcactgtcat	ctgttaggga	atttttgttt	gtcotgtott	tgcoctggatc	1550
catagcgaga	gtgctctgta	ttttttttta	gataatttgt	atttttgcac	1600
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 $\langle 211 \rangle$ 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	
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Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	
				20					25					30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	
				35					40					45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	
				50					55					60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	
				65					70					75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	
				80					85					90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	
				95					100					105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	
				110					115					120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	
				125					130					135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	
				140					145					150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	
				155					160					165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	
				170					175					180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	
				185					190					195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	
				200					205					210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	
				215					220					225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	
				230					235					240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	
				245					250					255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	
				260					265					270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
 275 280 285
 Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
 290 295 300
 Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
 305 310 315
 Arg Tyr Val Thr Lys Leu Leu Val
 320

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
 gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50
 cttcgcgata ttccgcgtta ccttcttgct ggcgttggtg ggagccgtgc 100
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200
 tttgcatgag ttctctggtta atttgcata gagatatggg cctgtggtct 250
 ccttctggtt tggcaggcgc ctcgtggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctotgaag 450
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa agaacgaaa aggaaggaac ttcagtcaac atattttcat 800
 tgactcctta gtacaagga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
tggtacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200
gatcgggttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
1				5					10					15
Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala
				20					25					30
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu
				35					40					45
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn
				50					55					60
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg
				65					70					75
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His
				80					85					90
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys
				95					100					105
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn
				110					115					120
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu
				125					130					135
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu

				140					145					150
Asp	Lys	Trp	Leu	Ser 155	Tyr	Pro	Glu	Thr	Gln 160	His	Val	Pro	Leu	Ser 165
Gln	His	Met	Leu	Gly 170	Phe	Ala	Met	Lys	Ser 175	Val	Thr	Gln	Met	Val 180
Met	Gly	Ser	Thr	Phe 185	Glu	Asp	Asp	Gln	Glu 190	Val	Ile	Arg	Phe	Gln 195
Lys	Asn	His	Gly	Thr 200	Val	Trp	Ser	Glu	Ile 205	Gly	Lys	Gly	Phe	Leu 210
Asp	Gly	Ser	Leu	Asp 215	Lys	Asn	Met	Thr	Arg 220	Lys	Lys	Gln	Tyr	Glu 225
Asp	Ala	Leu	Met	Gln 230	Leu	Glu	Ser	Val	Leu 235	Arg	Asn	Ile	Ile	Lys 240
Glu	Arg	Lys	Gly	Arg 245	Asn	Phe	Ser	Gln	His 250	Ile	Phe	Ile	Asp	Ser 255
Leu	Val	Gln	Gly	Asn 260	Leu	Asn	Asp	Gln	Gln 265	Ile	Leu	Glu	Asp	Ser 270
Met	Ile	Phe	Ser	Leu 275	Ala	Ser	Cys	Ile	Ile 280	Thr	Ala	Lys	Leu	Cys 285
Thr	Trp	Ala	Ile	Cys 290	Phe	Leu	Thr	Thr	Ser 295	Glu	Glu	Val	Gln	Lys 300
Lys	Leu	Tyr	Glu	Glu 305	Ile	Asn	Gln	Val	Phe 310	Gly	Asn	Gly	Pro	Val 315
Thr	Pro	Glu	Lys	Ile 320	Glu	Gln	Leu	Arg	Tyr 325	Cys	Gln	His	Val	Leu 330
Cys	Glu	Thr	Val	Arg 335	Thr	Ala	Lys	Leu	Thr 340	Pro	Val	Ser	Ala	Gln 345
Leu	Gln	Asp	Ile	Glu 350	Gly	Lys	Ile	Asp	Arg 355	Phe	Ile	Ile	Pro	Arg 360
Glu	Thr	Leu	Val	Leu 365	Tyr	Ala	Leu	Gly	Val 370	Val	Leu	Gln	Asp	Pro 375
Asn	Thr	Trp	Pro	Ser 380	Pro	His	Lys	Phe	Asp 385	Pro	Asp	Arg	Phe	Asp 390
Asp	Glu	Leu	Val	Met 395	Lys	Thr	Phe	Ser	Ser 400	Leu	Gly	Phe	Ser	Gly 405
Thr	Gln	Glu	Cys	Pro 410	Glu	Leu	Arg	Phe	Ala 415	Tyr	Met	Val	Thr	Thr 420
Val	Leu	Leu	Ser	Val 425	Leu	Val	Lys	Arg	Leu 430	His	Leu	Leu	Ser	Val 435

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
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cctgggctct cccagcctc cttcgactcg gagcggtca ggagacagaa 100
gaccggcct gctgcagccc catagtgtccc cggaacgagt ggaaggccct 150
ggcatcagag tgcgcccagc acctgagcct gcccttaagc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc agggctctact ggccctgcgggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcattcaga attggccaca 600
ctaccgtctc ccctgaggcc ctgctgatcc gcacccatt cctccctctc 650
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
<211> 196
<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	
1				5					10					15	
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	
			20						25					30	
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	
				35					40					45	
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	
			50						55					60	
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	
			65						70					75	
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	
			80						85					90	
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	
			95						100					105	
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	
			110						115					120	
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr	
			125						130					135	
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly	
			140						145					150	
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr	
			155						160					165	
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly	
			170						175					180	
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser	
			185						190					195	

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtccctcccgg ctcagaggac 150
cctgagcgtg atgaccacga gggccagccc cgccccggg tgcctcgga 200

gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250
tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
cccaaccgcc cgaaccacag cccccacccc tcagccaagg tgaagaaaat 350
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacggggcc gccggacctc gctttgcacc cacgacccag ccaagatctg 650
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tcaaagtcgt ctgtgtctac atcgccttct acagcacgga ctatcggctg 750
gtccagaagg tgtgcccaga ttacaactac catagtata cccctacta 800
cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850
ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900
gttgggcctc aggcaggag ggggggtggag acgaggagat gccagtggg 950
gccagggccca agtctcaagt ggcagagaaa ggggtcccaag tgctgggtccc 1000
aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050
ggctctctgt gcagcctcac agggctttgc cacggagoca cagagagatg 1100
ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
gtcatgggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200
gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
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gccagaggag ctctccagcc ctgcctagtg ggcgccctga gcccttgtc 1350
gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat 1400
gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450
ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca 1500
cccatcctta agctaagaca ggacgattgt ggtcctcca cactaaggcc 1550
acagcccatc cgcgtgctgt gtgtccctct tccaccccaa cccctgctgg 1600
ctcctctggg agcatccatg tccgggagag ggtccctca acagtcagcc 1650

tcacctgtca gaccgggggtt ctcccggatc tggatggcgc cgccctctca 1700
gcagcgggca cgggtggggc ggggccgggc cgcagagcat gtgctggatc 1750
tggtctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800
aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850
aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser	1	5	10	15
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser	20	25	30	
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	35	40	45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Prc	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210	

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

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			20					25						30
Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
			35					40						45
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
			50					55						60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
				200											

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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
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<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
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<210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
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<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
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ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	
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Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	
				20					25					30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
				50					55					60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95					100					105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
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Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226

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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20				25						30

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser		35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn		50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln		65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val		80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg		95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro		110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser		125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg		140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn		155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu		170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe		185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr		200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met		215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser		230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala		245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro		260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser		275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys		290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala		305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala				

	320		325		330
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala	335		340		345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly	350		355		360
Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser	365		370		375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe	380		385		390
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val	395		400		405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys	410		415		420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala	425		430		435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe	440		445		450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val	455		460		465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn	470		475		480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly	485		490		495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile	500		505		510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile	515		520		525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu	530		535		540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr	545		550		555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys	560		565		570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met	575		580		585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro	590		595		600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile	605		610		615

Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn
620 625 630

Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
635 640 645

Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu
650 655 660

Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
665 670 675

Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val
680 685 690

Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr
695 700 705

Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala
710 715 720

Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile
725 730 735

Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu
740 745 750

Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe
755 760 765

Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser
770 775 780

Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
785 790 795

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser
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Arg Asp Lys Ile Tyr Val Phe
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<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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<211> 807
<212> PRT
<213> Homo sapiens

<400> 229
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Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp					
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Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser					
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Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala					
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Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
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Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
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Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
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His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
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Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
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Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
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His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	
				320					325					330	
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	
				335					340					345	
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	
				350					355					360	
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	
				365					370					375	
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	
				380					385					390	
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	
				395					400					405	
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	
				410					415					420	
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	
				425					430					435	
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	
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Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	
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Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	
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Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	
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Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	
				500					505					510	
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	
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His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	
				530					535					540	
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	
				545					550					555	
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	
				560					565					570	
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	
				575					580					585	
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	
				590					595					600	
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly	

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Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp	
				620					625					630	
Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu	
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Gly	His	Gly	Pro	Tyr	Ser	Phe	Thr	Leu	Gly	Pro	Asn	Pro	Thr	Val	
				680					685					690	
Gln	Arg	Asp	Trp	Arg	Leu	Gln	Thr	Leu	Asn	Gly	Ser	His	Ala	Tyr	
				695					700					705	
Leu	Thr	Leu	Ala	Leu	His	Trp	Val	Glu	Pro	Arg	Glu	His	Ile	Ile	
				710					715					720	
Pro	Val	Val	Val	Ser	His	Asn	Ala	Gln	Met	Trp	Gln	Leu	Leu	Val	
				725					730					735	
Arg	Val	Ile	Val	Cys	Arg	Cys	Asn	Val	Glu	Gly	Gln	Cys	Met	Arg	
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Lys	Val	Gly	Arg	Met	Lys	Gly	Met	Pro	Thr	Lys	Leu	Ser	Ala	Val	
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Gly	Ile	Leu	Val	Gly	Thr	Leu	Val	Ala	Ile	Gly	Ile	Phe	Leu	Ile	
				770					775					780	
Leu	Ile	Phe	Thr	His	Trp	Thr	Met	Ser	Arg	Lys	Lys	Asp	Pro	Asp	
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<211> 50

<212> DNA

<213> Artificial

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<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

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<211> 24

<212> DNA

<213> Artificial Sequeunce

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 <223> Synthetic oligonucleotide probe

<400> 231
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<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

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<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

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				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

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<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys	1	5	10	15
Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr	20	25	30	
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr	35	40	45	
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val	50	55	60	
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val	65	70	75	
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr	80	85	90	
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr	95	100	105	
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser	110	115	120	
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala	125	130	135	
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly	140	145	150	
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe	155	160	165	
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys	170	175	180	
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp	185	190	195	
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala				

	200	205	210
Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe
	215	220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met
	230	235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu	Asn
	245	250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe
	260	265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala
	275	280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys
	290	295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser
	305	310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala
	320	325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser
	335	340	345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser
	350	355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile
	365	370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn
	380	385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile
	395	400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser	
	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagg 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tggtggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

agctgcccac gcctgagtc cagattcttc ccaggaacac aaacgtagga 100
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ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250
aaaggaaatg ttctccttat gtttgggtcta ctattgcatt tagaagctgc 300
aacaaattcc aatgagacta gcacctctgc caaactgga tccagtgtga 350
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
agtgggtcgc gcacagccac catctcaggg tccagcgtga cctccaatgg 450
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500
gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550
gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600
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cctccagtgg ggctagcaca gccaccaact ctgagtccag cacaacctcc 850
agtggggcca gcacagccac caactctgag tccagcacag tgtccagttag 900
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gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000
gccaccaact ctgagtccag cagcacctcc agtggggcca gcacagccac 1050
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gcaactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450
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caactctgac tccagcacia cctccagtga ggccagcaca gccaccaact 1550
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 aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250
 acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctagctctga 2300
 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
1				5				10						15
Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20				25						30
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35				40						45
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50				55						60
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65				70						75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85					90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				110					115					120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val
				125					130					135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				140					145					150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				155					160					165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				170					175					180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				185					190					195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				200					205					210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				215					220					225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				230					235					240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala
				245					250					255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				260					265					270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				275					280					285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				290					295					300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				305					310					315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala
				320					325					330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				335					340					345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				350					355					360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala

	365		370		375
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala		
	380	385	390		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr	Ala		
	395	400	405		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala		
	410	415	420		
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr	Ala		
	425	430	435		
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr	Val		
	440	445	450		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr	Ala		
	455	460	465		
Thr Asn Ser Gly	Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr	Ala		
	470	475	480		
Ala Leu Thr Gly	Met His Thr Thr Ser	His Ser Ala Ser Thr	Ala		
	485	490	495		
Val Ser Glu Ala	Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu	Ile		
	500	505	510		
Phe Leu Ile Thr	Leu Val Ser Val Val	Ala Ala Val Gly Leu	Phe		
	515	520	525		
Ala Gly Leu Phe	Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg	Asn		
	530	535	540		
Thr Phe Asn Thr	Ala Val Tyr His Pro	His Gly Leu Asn His	Gly		
	545	550	555		
Leu Gly Pro Gly	Pro Gly Gly Asn His	Gly Ala Pro His Arg	Pro		
	560	565	570		
Arg Trp Ser Pro	Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser	Ile		
	575	580	585		
Ala Met Glu Met	Ser Gly Arg Asn Ser	Gly Pro			
	590	595			

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct ggatggggcg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttgGCCa tggggtcaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa ctgggccaag ggggtcaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750
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acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850
gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950
tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	
1				5					10					15	
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	
				20					25					30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	
				35					40					45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	
				50					55					60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	
				65					70					75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	
				80					85					90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	
				95					100					105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	
				110					115					120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	
				125					130					135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	
				140					145					150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	
				155					160					165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	
				170					175					180	

Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
			200						205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
			215						220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
			230						235					240
Ser	Val	Ala	Asn	Ile	Met	Pro								
			245											

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaaggatc ttgaaggat caaccgaggg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

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cagtggacac tccaggaaga gcggccccgc ggggggcat gaccgtgcgc 100
tgaccctgac tactccagg tccggaggcg ggggcccccg gggcgactcg 150
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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu

80								85								90	
Phe	Ala	Leu	Ser	Ser 95	Asn	Leu	Ser	Phe	Leu 100	Pro	Gly	Gly	Glu	Tyr 105			
Gln	Glu	Leu	Leu	Trp 110	Gly	Ala	Asp	Ala	Glu 115	Lys	Lys	Gln	Gln	Cys 120			
Ser	Phe	Lys	Gly	Lys 125	Asp	Pro	Gln	Arg	Asp 130	Cys	Gln	Asn	Tyr	Ile 135			
Lys	Ile	Leu	Leu	Pro 140	Leu	Ser	Gly	Ser	His 145	Leu	Phe	Thr	Cys	Gly 150			
Thr	Ala	Ala	Phe	Ser 155	Pro	Met	Cys	Thr	Tyr 160	Ile	Asn	Met	Glu	Asn 165			
Phe	Thr	Leu	Ala	Arg 170	Asp	Glu	Lys	Gly	Asn 175	Val	Leu	Leu	Glu	Asp 180			
Gly	Lys	Gly	Arg	Cys 185	Pro	Phe	Asp	Pro	Asn 190	Phe	Lys	Ser	Thr	Ala 195			
Leu	Val	Val	Asp	Gly 200	Glu	Leu	Tyr	Thr	Gly 205	Thr	Val	Ser	Ser	Phe 210			
Gln	Gly	Asn	Asp	Pro 215	Ala	Ile	Ser	Arg	Ser 220	Gln	Ser	Leu	Arg	Pro 225			
Thr	Lys	Thr	Glu	Ser 230	Ser	Leu	Asn	Trp	Leu 235	Gln	Asp	Pro	Ala	Phe 240			
Val	Ala	Ser	Ala	Tyr 245	Ile	Pro	Glu	Ser	Leu 250	Gly	Ser	Leu	Gln	Gly 255			
Asp	Asp	Asp	Lys	Ile 260	Tyr	Phe	Phe	Phe	Ser 265	Glu	Thr	Gly	Gln	Glu 270			
Phe	Glu	Phe	Phe	Glu 275	Asn	Thr	Ile	Val	Ser 280	Arg	Ile	Ala	Arg	Ile 285			
Cys	Lys	Gly	Asp	Glu 290	Gly	Gly	Glu	Arg	Val 295	Leu	Gln	Gln	Arg	Trp 300			
Thr	Ser	Phe	Leu	Lys 305	Ala	Gln	Leu	Leu	Cys 310	Ser	Arg	Pro	Asp	Asp 315			
Gly	Phe	Pro	Phe	Asn 320	Val	Leu	Gln	Asp	Val 325	Phe	Thr	Leu	Ser	Pro 330			
Ser	Pro	Gln	Asp	Trp 335	Arg	Asp	Thr	Leu	Phe 340	Tyr	Gly	Val	Phe	Thr 345			
Ser	Gln	Trp	His	Arg 350	Gly	Thr	Thr	Glu	Gly 355	Ser	Ala	Val	Cys	Val 360			
Phe	Thr	Met	Lys	Asp 365	Val	Gln	Arg	Val	Phe 370	Ser	Gly	Leu	Tyr	Lys 375			

Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His	Pro
	380	385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala	Arg
	395	400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val	Leu
	410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg	Ser
	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val	Ala
	440	445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu	Phe
	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val	Gly
	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser	Gly
	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu	Leu
	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala	Asn
	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg	Asp
	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser	Leu
	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile	Glu
	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val	Ser
	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val	Gln
	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu	Ser
	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val	Asn
	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu	Leu
	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu	Glu
	650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val	Val

665	670	675
Glu Asp Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro
680	685	690
Val Ile Ile Ser	Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly Lys
695	700	705
Ala Ser Trp Gly	Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu Val
710	715	720
Met Cys Thr Leu	Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe
725	730	735
Leu Leu Tyr Arg	His Arg Asn Ser Met	Lys Val Phe Leu Lys Gln
740	745	750
Gly Glu Cys Ala	Ser Val His Pro Lys	Thr Cys Pro Val Val Leu
755	760	765
Pro Pro Glu Thr	Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser Thr
770	775	780
Pro Leu Asp His	Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro Pro
785	790	795
Gly Ala Arg Val	Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser Ile
800	805	810
Gln Asp Ser Phe	Val Glu Val Ser Pro	Val Cys Pro Arg Pro Arg
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Val Arg Leu Gly	Ser Glu Ile Arg Asp	Ser Val Val
830	835	

<210> 254
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 254
 agcccggtgca gaatctgctc ctgg 24

<210> 255
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 <212> DNA
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<220>
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<400> 255
tgaagccagg gcagcgtcct ctgg 24

<210> 256
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<212> DNA
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<220>
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<400> 256
gtacaggctg cagttggc 18

<210> 257
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<212> DNA
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<220>
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<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
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<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
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agggcgggac gggagcccgg actcgtctgc cgccgcgctc gtcgccgtcg 150

tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cggcacctcg 200
 cggccgagcc gccgctagcg cgcgccgggc atggtcccct cttaaaggcg 250
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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

	530		535		540
Ser Gly Arg Phe	Asp 545	Met Phe Val Arg	Phe 550	Met Gly Asn Phe	Glu 555
Lys Thr Cys Leu	Ile 560	Pro Asn Gln Asn	Val 565	Lys Leu Val Val	Leu 570
Leu Phe Asn Ser	Asp 575	Ser Asn Pro Asp	Lys 580	Ala Lys Gln Val	Glu 585
Leu Met Arg Asp	Tyr 590	Arg Ile Lys Tyr	Pro 595	Lys Ala Asp Met	Gln 600
Ile Leu Pro Val	Ser 605	Gly Glu Phe Ser	Arg 610	Ala Leu Ala Leu	Glu 615
Val Gly Ser Ser	Gln 620	Phe Asn Asn Glu	Ser 625	Leu Leu Phe Phe	Cys 630
Asp Val Asp Leu	Val 635	Phe Thr Thr Glu	Phe 640	Leu Gln Arg Cys	Arg 645
Ala Asn Thr Val	Leu 650	Gly Gln Gln Ile	Tyr 655	Phe Pro Ile Ile	Phe 660
Ser Gln Tyr Asp	Pro 665	Lys Ile Val Tyr	Ser 670	Gly Lys Val Pro	Ser 675
Asp Asn His Phe	Ala 680	Phe Thr Gln Lys	Thr 685	Gly Phe Trp Arg	Asn 690
Tyr Gly Phe Gly	Ile 695	Thr Cys Ile Tyr	Lys 700	Gly Asp Leu Val	Arg 705
Val Gly Gly Phe	Asp 710	Val Ser Ile Gln	Gly 715	Trp Gly Leu Glu	Asp 720
Val Asp Leu Phe	Asn 725	Lys Val Val Gln	Ala 730	Gly Leu Lys Thr	Phe 735
Arg Ser Gln Glu	Val 740	Gly Val Val His	Val 745	His His Pro Val	Phe 750
Cys Asp Pro Asn	Leu 755	Asp Pro Lys Gln	Tyr 760	Lys Met Cys Leu	Gly 765
Ser Lys Ala Ser	Thr 770	Tyr Gly Ser Thr	Gln 775	Gln Leu Ala Glu	Met 780
Trp Leu Glu Lys	Asn 785	Asp Pro Ser Tyr	Ser 790	Lys Ser Ser Asn	Asn 795
Asn Gly Ser Val	Arg 800	Thr Ala			

<210> 261
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30
Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45
Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser

Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys	50	55	60
65	70	75	
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu	80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335	340	345

Leu Leu Lys Val Tyr
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<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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aaa 2403

<210> 267
<211> 466
<212> PRT
<213> Homo sapiens

<400> 267
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Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu					
				35					40					45					
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe					
				50					55					60					
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser					
				65					70					75					
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp					
				80					85					90					
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr					
				95					100					105					
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile					
				110					115					120					
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly					
				125					130					135					
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile					
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Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala					
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Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg					
				170					175					180					
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile					
				185					190					195					
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu					
				200					205					210					
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu					
				215					220					225					
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu					
				230					235					240					
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile					
				245					250					255					
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp					
				260					265					270					
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys					
				275					280					285					
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys					
				290					295					300					
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro					
				305					310					315					

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

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<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
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<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269

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Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr	35	40	45	
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr	50	55	60	
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn	65	70	75	
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala	80	85	90	
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val	95	100	105	
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu	110	115	120	
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp	125	130	135	
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val	140	145	150	
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile	155	160	165	
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr	170	175	180	
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly	185	190	195	
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	200	205	210	
Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	215	220	225	

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230					235					240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250					255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280					285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295					300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310					315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355					360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
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Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
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20 25 30
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
95 100 105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
110 115 120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
125 130 135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
140 145 150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
155 160 165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
170 175 180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
185 190 195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
200 205 210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
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Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
230 235

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
				125					130					135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
				140					145					150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155					160					165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser

				170						175					180
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	
				185					190					195	
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	
				200					205					210	
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	
				215					220					225	
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	
				230					235					240	
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	
				245					250					255	
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	
				260					265					270	
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	
				275					280					285	
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	
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				305											

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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cttgggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200

agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250

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aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350

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cgggcagcct ctccacttca tcccaggagaa gcagctgtgt gacggagagc 450

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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

265

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Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala Lys	260	265	270
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn Asp	275	280	285
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly Thr	290	295	300
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr Pro	305	310	315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln Asn	320	325	330
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln Val	335	340	345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly Glu	350	355	360
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly Val	365	370	375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln Ser	380	385	390
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly Cys	395	400	405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr	Thr Lys Val Ser Ala Tyr	410	415	420
Leu Asn Trp Ile	Tyr Asn Val Trp Lys	Ala Glu Leu	425	430	

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

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Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln	Val		
	320		325		330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu	Asp		
	335		340		345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys	Glu		
	350		355		360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro	Arg		
	365		370		375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu	Thr		
	380		385		390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly	Thr		
	395		400		405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala	Val		
	410		415		420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met	Tyr		
	425		430		435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser	Gly		
	440		445		450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro	Asp		
	455		460		465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly	Ala		
	470		475		480
Val Phe Val Gly	Phe Ser Gly Gly Val	Trp Arg Val Pro Arg	Ala		
	485		490		495
Asn Cys Ser Val	Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala	Arg		
	500		505		510
Asp Pro His Cys	Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys	Leu		
	515		520		525
Leu Ser Ala Pro	Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu	Arg		
	530		535		540
Gly Asn Pro Glu	Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg	Ser		
	545		550		555
Leu Arg Pro Gln	Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu	Ala		
	560		565		570
Val Pro Asn Ser	Ile Leu Glu Leu Pro	Cys Pro His Leu Ser	Ala		
	575		580		585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 278
ctgctggtga aatctggcgt ggag 24

<210> 279
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 279
gtctgtgcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtogetcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
aggggtccctt agccggggcg agggcgcgca gcccaggctg agatccgcgg 50
cttccgtaga agtgagcatg gctgggcagc gagtgcttct tctagtgggc 100
ttcctttctcc ctggggtcct gctctcagag gctgccaaaa tcttgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaagagaa ctgcgacatg gtgatagttg 500
aaacttttga ctactgtcct ttcttgattg ctgagaagct tgggaagcca 550
tttgtggcca ttctttccac ttcatcggc tctttggaat ttgggctacc 600
aatccccttg tcttatgttc cagtattccg ttccctgtg actgatcaca 650
tggaacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750
tttcacagaa ggctctaggc cagttttgtc tcatcttcta ctgaaagcag 800
agttgtgggt cattaactct gactttgcct ttgatattgc tcgacctctg 850
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

agtaccacaa gacttggaga acttcattgc caagtttggg gactctgggt 950
 ttgtccttgt gaccttgggc tccatggtga acacctgtca gaatccggaa 1000
 atcttcaagg agatgaacaa tgcctttgct cacctacccc aaggggtgat 1050
 atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100
 atgtgaaaat tgtggactgg cttcctcaga gtgacctoct ggctcaccca 1150
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 catccagcat ggtgtgcccc tgggtgggat ccctctcttt ggagaccagc 1250
 ctgaaaacat ggtccgagta gaagccaaaa agtttgggtgt ttctattcag 1300
 ttaaagaagc tcaaggcaga gacattggct cttaatgaatga aacaaatcat 1350
 ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcacacctgc 1400
 gctcccaccc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450
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 gattctgtct ctgagtgact tggaccactg accctcagat ttccagcctt 1950
 aaaatccacc ttctttctca tgcgcctctc cgaatcacac cctgactctt 2000
 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050
 atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100
 ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150
 tgtgcttgag agttcagggc cggacacagg ctcacaggtc tccacattgg 2200
 gtccctgtct ctgggtgcca cagtgaagctc cttcttggct gagcaggcat 2250
 ggagactgta ggtttccaga tttcctgaaa aataaaaagtt tacagcgtta 2300
 tctctcccca acctcactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
1				5					10					15
Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 285
 cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50
 gggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
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 gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
 cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250
 tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300
 gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
 gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400
 ccaggagag gagcggaac agaagagggg cagaagaccg gggcacttgt 450

gggttgcaga gccctcagc catgttggga gccaagccac actggctacc 500
 aggtccccta cacagtcccg ggctgccctt ggttctggtg cttctggccc 550
 tgggggcccg gtgggccag gaggggtcag agcccgctct gctggagggg 600
 gagtgcctgg tggctgtga gcctggccga gctgctgcag gggggcccg 650
 gggagcagcc ctgggagagg cccccctgg gcgagtggca tttgctgcgg 700
 tccgaagcca ccacatgag ccagcagggg aaaccggcaa tggcaccagt 750
 ggggccatct acttcgacca ggtcctggtg aacgagggcg gtggctttga 800
 ccgggcctct ggctccttcg tagccctgt ccgggggtgc tacagcttcc 850
 ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900
 atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950
 gaccggggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000
 accgagtgtc tctgcgctg cgctggggga atctactggg tggttgaaa 1050
 tactcaagtt tctctggctt cctcatcttc cctctctgag gaccaagtc 1100
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 gagctgtggc atctccagac caggcctttc caccaccca ccccagtta 1300
 ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350
 ggcaagggtt ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400
 ctccggttcc cccacccag cttctgctc aatgctgatc agggacaggt 1450
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 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550
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 aggctcagcc acaggcagaa gggtggaag ggctggagt ctgtggctgg 1650
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ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
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 tcttatcccg ctgtcccatt ggcccagcct ggatgaatct atcaataaaa 2200
 caactagaga atgggtggta gtgagacact atagaattac taaggagaag 2250
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cgggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctacggagg acctgcgctg tcgcgcgagg ggtctgggag 300
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 gtgctccagt gggtcctgtc ctcccttgta ctgggagtggt cctgcagtgc 450
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 aggtcacagt gggtcgaaa ctgggtgtgt tggcgctact ttcgagacta 600
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 atatcttttg ataccacccc catggtatca tgggcctggg tgccttctgc 700
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 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1550
 aaaaaaaaa aaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
1				5					10					15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
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gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggccgtg 250
caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350
tcatcaactt cgtccagctg tgacgcctgg cgctctggcc ggtcagcaag 400
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
actggtcatg ctgctggagt ggtggtcctg cacggagtgt acactgttca 500
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550
ctcaaccaca acttcgagat cgacttctc tgtgggtgga ccatgtgtga 600
gcgcttcgga gtgctgggga gctccaaggt cctcgctaag aaggagctgc 650
tctacgtgcc cctcatcgcc tggacgtggt actttctgga gattgtgttc 700
tgcaagcgga agtgggagga ggaccgggac accgtggctg aagggtgag 750
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800
ggacgcgctt cacggagacc aagcaccgcg ttagcatgga ggtggcggct 850
gctaaggggc ttctgtcct caagtaccac ctgctgccgc ggaccaaggg 900
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atgtaaccct gaacttcaga ggaaacaaga acccgctcct gctggggatc 1000
ctctacggga agaagtacga ggcggacatg tgcgtagga gatttcctct 1050
ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaaggcatg 1150

tttccagggg agcagtttaa gcctgcccgaggccgtgga ccctcctgaa 1200
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 tttgtgggag cagcttcctt tggagtctgc agactgatag gagaatcgct 1350
 tgaacctggg aggtggagat tgcagtgagc tgagatggca tcactgtact 1400
 ccagcctagg caacagagca agactcagtc tcaaaaaaaaa aaaaaaaca 1450
 aaaaacccca gaaattctgg agttgaactg tgtagttact gacatgaaaa 1500
 attcactaga ggctgaacag cagatttgag caggcagaaa aaaatcagca 1550
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 aggaaaatta acagcctcag agacccatgg tgcaccgtca cacaatatca 1650
 catatgcatg atgagagtcc cagaaggaga ggagagaaag ggtcagaaag 1700
 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
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 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtccctgacct 2000
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100
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 ggggtcaggc tgatctcaaa ctctgagtt caggtgatct gcccgctca 2200
 gcctcccaaa gtgttgtgat tgcaggcgtg agccactgcg cctggccgga 2250
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 gtgatoccaa gtagcttgga ttgtaaacat gcaccacat gcctggctaa 2350
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 cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500
 atttgtatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 2550
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 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gccccaacta 2950
 ccaggagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000
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 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccoct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

gatattcttt atttttaaga atctgaagta ctatgcatca ctccctccaa 50

tgtcctgggg cagccaccag gcatattcat ctttgttgtt gtttttcttt 100

tgcttttagca ctggggcact tcttgcttat ttcttttgga ggaaaggggc 150

tcagtttgtc ttgtgggggtt ggtggcaggc aggccggctt acgcctgata 200

cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250

tagctgggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300

ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350

ttctctctgt tcttaggata aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450

tgtcgttcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500

tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550

atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600

ctggcctgac agaatctcat cttgttttaat gctctcataa gaccacttgt 650

ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700

gttgatatggg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750

agggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg ccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggtoct gattcagtag 950
 gccaggttg ggcattctta acaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
 tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgac 1100
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacaca attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggagggtg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5				10						15
His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20				25						30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35				40						45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50				55						60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65				70						75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80				85						90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95				100						105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110				115						120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125				130						135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
 ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50
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 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350
 ctctcgctgg agcagtggcc tcaccaactg tctcacgtct ggaggcactg 400
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
 tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500
 ggcgatggct cccactgccc aggcacacgc cttgctgtag tcaatcactg 550
 ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600
 acatcacgct gcccgcccat ctaacotttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700
 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750
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 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850
 gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900
 ggaagggtcg ccgatggcg atgacacact cgggactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000
 ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050
 ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc 1100
 ctccccctcct tccctctgag aggcctcct atgtccctac taaagccacc 1150
 agcaagacat agctgacagg ggctaattgg tcagtgttgg ccaggaggt 1200
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tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350
 agctagagct tggttcaaat gatctccaag ggcccttata cccaggaga 1400
 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccagggtgcat 1450
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 gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc 1600
 aggcattggt gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750
 aattatggtt atttgtaa 1768

<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser
 1 5 10 15
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

gcgggcccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50
 tgtcactgcc tcccgcgcgc tctgtcccgc gccatgaccc agccggtgcc 100
 ccggctctcc gtgcccgcgc cgtgtggcctt gggctcagcc gcactgggcg 150
 ccgccttcgc cactggcctc ttcctgggga ggcggtgccc cccatggcga 200
 ggccggcgag agcagtgcct gcttcccccc gagggacagcc gcctgtggca 250
 gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300
 ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350
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 cgctgcccgc ggacgggagc gtggtgacct gcgaggtgga cgcgcagccc 500
 ccggagctgg gacggcccct gtggaggcag gccgaggcgg agcacaagat 550
 cgacctcgg ctgaagccc ccttgagagc cctggacgag ctgctggcgg 600
 cgggagcagg cggcacctc gacgtggcgc tgggtgatgc ggacaaggag 650
 aactgctccg cctactacga gcgctgcctg cagctgctgc gaccggagg 700
 catcctcgcc gtctcagag tctgtggcg cggaagggtg ctgcaacctc 750
 cgaaagggga cgtggcgccc gagtgtgtgc gaaacctaaa cgaacgcac 800
 cggcgaggag tcagggtcta catcagcctc ctgcccctgg gcgatggact 850
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 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
1				5					10					15
Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
			20						25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
			35						40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
			50						55					60

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
65 70 75

Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
80 85 90

Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
95 100 105

Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
110 115 120

Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
125 130 135

Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
140 145 150

Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
155 160 165

Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
170 175 180

Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
185 190 195

Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
200 205 210

Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
215 220 225

Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
230 235 240

Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
245 250 255

Leu Thr Leu Ala Phe Lys Ile
260

<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

ccgccgccgc agccgctacc gccgctgcag ccgctttccg cggcctgggc 50

ctctcgccgt cagcatgccca cagccttca agcccgggga cttggtgttc 100

gctaagatga agggctaccc tactggcct gccaggatcg acgacatcgc 150

ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200

gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

tcaagtgcgc ggtcctcggc ccaaagatcg aggcggtgca gaaagtgaac 1750
aaggctggga tggagaagga gaaggccgag gagaagctgg ccggggagga 1800
gctggccggg gaggaggccc ccaggagaa ggcggaggac aagcccagca 1850
ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900
agcgcagagg acaaggagca cgaggagggc cgggactcgg aggagggggc 1950
aaggtgtggc tcctctgaag acctgcacga cagcgtagcg gaggggtccc 2000
acctggacag gcctgggagc gaccggcagg agcgcgagag ggcacggggg 2050
gactcggagg ccctggacga ggagagctga gccgcgggca gccaggccca 2100
gccccgcgcc gagctcaggc tgcccctctc ottccccggc tcgcaggaga 2150
gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttccctt 2200
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actataaacg gttttttaat ga 2272

<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
1				5					10					15
Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
				50					55					60
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
				80					85					90
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

	140		145		150
Asp Asn Ser Gly	Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met	Ser		
	155	160	165		
Val Ser Lys Arg	Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln	Ala		
	170	175	180		
Ser Val Ser Pro	Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser	Glu		
	185	190	195		
Ser Glu Lys Thr	Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys	Ala		
	200	205	210		
Ala Val Arg Ala	Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys	Lys		
	215	220	225		
Lys Lys Ala Pro	Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp	Ser		
	230	235	240		
Asp Gly Ala Lys	Pro Glu Pro Val Ala	Met Ala Arg Ser Ala	Ser		
	245	250	255		
Ser Ser Ser Ser	Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser	Val		
	260	265	270		
Lys Lys Pro Pro	Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu	Pro		
	275	280	285		
Lys Pro Arg Gly	Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser	Ser		
	290	295	300		
Ser Ser Ser Asp	Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser	Glu		
	305	310	315		
Trp Lys Arg Arg	Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala	Arg		
	320	325	330		
Arg Arg Arg Glu	Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu	Gln		
	335	340	345		
Glu Lys Glu Glu	Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg	Gly		
	350	355	360		
Glu Ala Glu Arg	Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu	Arg		
	365	370	375		
Glu Asp Asp Glu	Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg	Gly		
	380	385	390		
Arg Gly Pro Pro	Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu	Leu		
	395	400	405		
Glu Arg Glu Ala	Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser	Ser		
	410	415	420		
Thr Glu Pro Ala	Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val	Arg		
	425	430	435		

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
440 445 450

Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
455 460 465

Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
470 475 480

Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
485 490 495

Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Leu	Lys	Cys	Pro	Phe 185	Asp	Pro	Gln	Gln	Pro 190	Phe	Ala	Ser	Val	Met 195				
Thr	Asp	Glu	Tyr	Leu 200	Tyr	Ser	Gly	Thr	Ala 205	Ser	Asp	Phe	Leu	Gly 210				
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His	Tyr	Ile	Arg	Thr 230	Asp	Ile	Ser	Glu	His 235	Tyr	Trp	Leu	Asn	Gly 240				
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Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
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Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu		170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu		185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser		200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu		215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln		230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu		275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu		290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala				

				305					310					315
Pro	Thr	Ser	Val	Leu	Asp	Gly	Pro	Pro	Ala	Pro	Val	Leu	Pro	Gly
				320					325					330
Asp	Lys	Ala	Leu	Asp	Phe	Pro	Gly	Phe	Leu	Asp	Met	Met	Ala	Pro
				335					340					345
Arg	Leu	Arg	Pro	Met	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Lys	Ala
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<210> 316
<211> 4407
<212> DNA
<213> Homo sapiens
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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro
			20						25					30
Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu
			35						40					45
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
			50						55					60
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
			65						70					75
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
			80						85					90
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
			95						100					105
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
			110						115					120
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
			125						130					135
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu

	140		145		150
Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro Leu	155		160		165
Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile	170		175		180
Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn	185		190		195
Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala	200		205		210
Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val	215		220		225
Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg	230		235		240
Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His	245		250		255
Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val	260		265		270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala	275		280		285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn	290		295		300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu	305		310		315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu	320		325		330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys	335		340		345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala	350		355		360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys	365		370		375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val	380		385		390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser	395		400		405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr	410		415		420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro	425		430		435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln	440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro	455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala	470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys	485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp	500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro	515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val	530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly	545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn	560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe	590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro	605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr	620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser	635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys	665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly	680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile	695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser			

	725		730		735									
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp
				740					745					750
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr
				755					760					765
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro
				770					775					780
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg
				785					790					795
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro
				800					805					810
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu
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Glu	Ile	Leu	Arg	Arg	Arg	Pro	Trp	Ala	Gly	Arg	Lys			
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<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cggatgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgogcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
				20					25					30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
				35					40					45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50					55					60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
				65					70					75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
				80					85					90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95					100					105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110					115					120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125					130					135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140					145					150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155					160					165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170					175					180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185					190					195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
				200					205					210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215					220					225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230					235					240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245					250					255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260					265					270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
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 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
 aaccccgctca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttcagc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350
 gtcctgggtg ccattggcct cctggtatcc atctttgccc tgaaatgcat 400
 ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
 gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550
 gtacaccggc atgggtggga tggcgcagac tgttcagacc aggtacacat 600
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
 gggggtgtga tgatgtgcat cgctgccgg ggctggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
 aagaagatat acgatggagg tgccgcaca gaggaagagg tacaatctta 850
 tccttccaag cagcactatg tgtaatgctc taagacctct cagcacgggc 900
 ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
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tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
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 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cggttttctt aactgtgat cttaaaagtt accaaaccaa 1450
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500
 tcttattaca gcaacacccat tctaggaggt tctgagctc tccactggag 1550
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggagggtt gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
 1 5 10 15

Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20 25 30

Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45

Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60

Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75

Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe	Ala Leu Lys Cys Ile Arg	
95	100	105
Ile Gly Ser Met Glu Asp Ser Ala Lys	Ala Asn Met Thr Leu Thr	
110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly	Leu Cys Ala Ile Ala Gly	
125	130	135
Val Ser Val Phe Ala Asn Met Leu Val	Thr Asn Phe Trp Met Ser	
140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly	Gly Met Val Gln Thr Val	
155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala	Leu Phe Val Gly Trp Val	
170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly	Val Met Met Cys Ile Ala	
185	190	195
Cys Arg Gly Leu Ala Pro Glu Glu Thr	Asn Tyr Lys Ala Val Ser	
200	205	210
Tyr His Ala Ser Gly His Ser Val Ala	Tyr Lys Pro Gly Gly Phe	
215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn	Thr Lys Asn Lys Lys Ile	
230	235	240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp	Glu Val Gln Ser Tyr Pro	
245	250	255
Ser Lys His Asp Tyr Val		
260		

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
 ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50
 gtagcagttc cggagtccag ctggctaaaa ctcattccag aggataatgg 100
 caacccatgc ottagaaatc gctgggctgt ttcttggtgg tgttggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggcttt catgatggcc atccttggca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgaagg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 cctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactgggtgt gattgttggg ggagctctgt tctgctgcgt 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atgcacaaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tactttotca aaatggaccc 850
 caaagaaact ttgatttact gttcttaact gcctaattct aattacagga 900
 actgtgcata agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctcatataga gacatgctta 1150
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgcttttcag ggaaatcatg gataggggtg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct ccagaggct ttttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaaagt tgatctaaga aaaagtgatg 1550
 gttttaggaa agtgaataa tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgc taccaaaaaa acaacaacaa aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttggttc tgtgaaaaat aaatttcctt ctgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc ttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly
 1 5 10 15
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
 20 25 30
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
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 ctgggctggg tgaatggcct ggtctcctgt gccctgcca tgtggaaggt 100
 gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150
 gcctgtggat gtctgctgt gtgcagagca ccggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgctggggc caagtgtacc acctgtgtg aggagaagga ttccaaggcc 350
 cgcttggtgc tcacctctgg gattgtcttt gtcattctcag gggctctgac 400
 gctaattccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggg ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg ccttttgttg ctgggtgggg ggttgctgtg 550
 ctgcacttgc ccctcggggg ggtcccagg cccagccat tacatggccc 600
 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750
 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
 gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900
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 agagttcctg ctgctgctgg gggctgggct tccctagatg tactggaca 1050
 gctgcccccc atcctactca ggtctctgga gctcctctct tacccttg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250

gccccctcg tctaccccc ttacactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

gccaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50
ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100
gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
gttccttggc atgggtggga ctcttgccac aacccttctg cctcagtggg 200
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
ggaagggctc tggatgaatt gcatccgaca agccaggggc cggttgcaat 300
gcaagttcta tagctccttg ttggctctcc cgcctgccct ggaaacagcc 350
cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccttgcttat 400
tggcatctgt ggcataaagc aggtccagtg cacaggctct aacgagaggg 450
ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
atcttcgttc tgattccggt gagctggaca gccaatataa tcatacagaga 550
tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600
cacttttcct tggctgggca agcgtctgtg tcctcttcat tggagggggg 650
ctgctttgtg gattttgctg ctgcaacaga aagaagcaag ggtacagata 700
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttatg tctaatgcct ccttttggct 800
ccaagtatgg actatggtca atgtttttta taaagtctg ctagaaactg 850
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
cgaaagtttc aatttgttac tgggtgtagg aatgaaaatg acttacttgg 950
acattctgac ttcaggtgta ttaaagcat tgactattgt tggacccaat 1000
cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50

atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100

ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150

agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200

tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250

gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300

aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350

tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400

ggtggggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgcccg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

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tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcatgtatc tcctaatagcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly	1	5	10	15
Leu	Ala	Leu	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser	20	25	30	
Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val	35	40	45	
Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu	50	55	60	
Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg	65	70	75	
Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met	80	85	90	
Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu	95	100	105	
Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln	110	115	120	
Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr	125	130	135	
Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr	140	145				

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337

cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50
agccggggcgc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100
tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gaccactgc ccagccgtc agggaccca acgccaatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350
 ggggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450
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 cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
 tgtccacgag agtcgggtccc ccaaattccc cctgcccgcc ggggtccgag 650
 cccggccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
 ttcccttgac cgccactctg ggccctggccg gcttcaccct gctcctcagt 800
 ctctggcct ttgccatgta ccgcccgtag tgccctccgc ggcgcttggc 850
 agcgtcgccg gcccctccgg accttgctcc ccgcgccgcg gcgggagctg 900
 ctgcctgccc agggccgcct ctccggcctg cctcttcccg ctgccctgga 950
 gccagccct gcgccgcaga ggactcccgg gactggcgga ggccccgcc 1000
 tgcgaccgcc ggggtcggg gccacctccc ggggtgctg aacctcagcc 1050
 cgcactggga gtgggctcct cggggtcggg catctgctgt cgctgcctcg 1100
 gccccgggca gagccgggcc gccccggggg cccgtcttag tgttctgccg 1150
 gaggaccag ccgcctcaa tccctgacag ctcttgggc tgagttgggg 1200
 acgccaggtc ggtgggaggc tggggaagg gagcggggag gggcagagga 1250
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaaa 1300
 aaaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
1				5					10					15
Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25					30
Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35					40					45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50

tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100

caagacccta agaaccatca gccctcagct gcacctcctc ccctccaagg 150

atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
tggaagcttt gactatggcc tttccagat caacagccac tactggtgca 400
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
ctgtctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
gtccggagca cgggggatga acaactgggt agaattggagg ttgcactgtt 550
caggccggcc actctctac tggctgacag gatgccgcct gagatgaaac 600
aggggtgcggg tgcacgtgg agtcattcca agactcctgt cctcactcag 650
ggattottca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
ccttcccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750
tcttggttc ctcttactc ccactctggac ccagtccct ggttcctgtc 800
tggtatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg		

<210> 341
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 341
 ccctccaagg atgacaaagg cgc 23

<210> 342
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-29
 <223> Synthetic construct.

<400> 342
 ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 343
 atctcaggcg gcatcctgtc agcc 24

<210> 344
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 344
 gtggatgcct gcaagaaggt tggg 24

<210> 345
 <211> 45
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
agcttttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
actgagaacc caccagctca tcccagacac ctcatagcaa cctattttata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa ccggggtaaa gggagggaaag caattcaatt tgaagtccct 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
gggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
ttgcacacgc tgttggaaca tgtcaggacc aggttaagtg actggcagaa 350
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgga 450
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatgg 550
ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600
aagccagcaa gcacagccct gaagccagggt accgcctgga ctttggggaa 650
tcccaggatt gggactgga agctgaggat gaggggtgaag agtacagccc 700
tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750
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cccaaagagg gactgggggg ctgatgagga cggggagggtg tctgaagaag 900
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tcagcagaat agctgggtgac aggagccgag tggatatctc ggtgatagat 1400
gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450
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atatatttca tgaagctgat cttttgtgt gtgtgctcct tgtgttagga 2500
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tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
1 5 10 15

Phe Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

	545		550		555
Gly Ser Pro Gln	His Leu Cys Phe Ala	Val Arg Gln Glu Gln	Val		
	560		565		570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly	Leu Ala Ile His Gln	Gln		
	575		580		585
His Trp Asp Phe	Gln Glu Asn Gly Met	Ile Val His Ile Leu	Ser		
	590		595		600
Gly Lys Cys Met	Glu Ala Val Val Gln	Glu Asn Asn Lys Asp	Leu		
	605		610		615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg	Phe		
	620		625		630
Asp Gln Ile Asn	Ala Val Asp Glu Arg				
	635				

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 348
 ggagaggtgg tggccatgga cag 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 350
 tatgtcgctg cgaggtgggtg aaaacctcga actgtctttc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
ctcagacatg gaggccagga tgtggcctgc gctgctgctg tcccacctcc 100
tccctctctg gccactgctg ttgctgcccc tcccacgccc tgctcagggc 150
tcttcatact cccctcgaac cccaccagcc ccagcccgcc ccccggtgtg 200
caggggaggc ccctcggccc cacgtcatgt gtgogtgtgg gagcgagcac 250
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300
cctggcactg cccccccagc cccccatca ggctttgagg agggggccgcc 350
ctcatcccaa taccctggg ctatcgtgtg gggcccacc gtgtctcgag 400
aggatggagg ggacccaac tctgccaatc cgggatttct ggactatggt 450
tttgagccc ctcatgggct cgcaacccca caccccaact cagactccat 500
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600
gtcacaatta ccattctcat catcattgtt ctctgggcca ctggcatcat 650
cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700
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ccaagcagga ggccaagggg ccggcacagc ccccatccca ctgaggggtgg 1350
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 cacaccaccc ggaacactcc ccagccccac gggcaatcct atctgctcgc 1450
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 tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
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tctccaagaa gttctccttc taccgccacc atgtgaactt caagtccctg 200
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggttat ttccccaacg agctgcgaaa 400
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agaggagggg ggctaggggg tcctctagat cagtgggggc actgcaggtg 1450
gggctctccc tatacctggg acaoctgctg gatgtcacct ctgcaaccac 1500
acccatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550

Ser Pro Arg Gly Asp Leu Pro
155

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<210> 357
<211> 1536
<212> DNA
<213> Homo sapiens
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<400> 357
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acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
gcatgggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggtttctga cactacaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
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agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctctttattc tgggtggacag tggtatgaaa gaaaatggga aggtgatatc 650
atctttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat aactgocca cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaatat tgttgaaaga 800
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tctcttcttc ottcttttaa atttcatatc ctcactccct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

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ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
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cagaagttaa aggcgtgtctc caagtccctg aactcagcag aaatagacca 1450
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caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccca ggcgagccaa 100
cctcagcggg gacccgggct cagggacgcg gcggcggcgg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggg gctggcggcg gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgcgtagaa aaagagaatt tgctgtgttt 650
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tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile
				110					115					120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys
				125					130					135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile
				140					145					150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val
				155					160					165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr
				170					175					180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn
				185					190					195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser
				200					205					210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly
				215					220					225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile
				230					235					240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile
				245					250					255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn	
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<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggcc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtcccccgcg gcccccgacc ctgaggcgctc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300
agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggttttag 450
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cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaaggtg aaaagggtttc tgtcacaaca 650
 agattactga tttcccatTT aagtggaatt cgtcattatg aaaaggacat 700
 aaaaaaggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
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 caggaagaaa acgagccagt gatttacaat agagcaaggT aaatgaatac 1150
 cttctgctgt gtctagctat atcgcacTct aacactatTT tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaaoctgc cacatttttgg 1250
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 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
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Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
 20 25 30

Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
 35 40 45

Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
 50 55 60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
 65 70 75

Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
 80 85 90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	
				95					100					105	
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	
				110					115					120	
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	
				125					130					135	
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	
				140					145					150	
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	
				155					160					165	
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	
				170					175					180	
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	
				185					190					195	
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	
				200					205					210	
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	
				215					220					225	
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	
				230					235					240	
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	
				245					250					255	
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	
				260					265					270	
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	
				275					280					285	
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	
				290					295					300	
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	
				305					310					315	
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	
				320					325					330	
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	
				335					340					345	
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	
				350					355					360	
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			
				365					370						

<210> 367

<211> 30
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-30
 <223> Synthetic construct.

<400> 367
 tggaaaagaa gtctgggtcag aaggtttagg 30

<210> 368
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 368
 catttggctt cattctcctg ctctg 25

<210> 369
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 369
 aaaacctcag aacaactcat tttgcacc 28

<210> 370
 <211> 41
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-41
 <223> Synthetic construct.

<400> 370
 gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
 <211> 1150
 <212> DNA
 <213> Homo sapiens

<400> 371
 gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200
tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
tactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
gaagctggtg gctatgtctc ctcccttctc cctgcgtgct ccctggtgga 500
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<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

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Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
			35						40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
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 cagcaggtcg tccggggggc caccatgctg gtgactgcct accttgcttt 150
 tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

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ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
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cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
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tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttcttaogga gaaaggtgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttcogg gtacctctgc actcactggc ttgcctaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgcccctga gctgtaacct cactccagga caagatagct 1500
gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
gggaggacat gatgggggtg atggactgga aagaagggtc caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac acttttaa at gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15

Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45

Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60

Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75

Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90

Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105

Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120

Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135

Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150

Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165

Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180

Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195

Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225

Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	
				365					370					375	
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	
				380					385					390	
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	
				395					400					405	
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	
				410					415					420	
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	
				425					430					435	
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	
				440					445					450	

<210> 375
 <211> 1098
 <212> DNA
 <213> Artificial

<400> 375
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgcccg gccgggcccg 50
 gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100
 gctccccgcg tgcgtcgcg cccacggctt ccgtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacgggt 300
 tottcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
 ctctccaaga ctcggttggt ccaggagcac ggcgggcggg cggtgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca ggcacacagct gacatccccg cctcttctct gctcggccga 500
 gacggctaca tgatccgcgc ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atccagtcga atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtcca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgagaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750
 tttgggcgtt gctaggctga aaggaagcc acaccactgg cttcccttc 800
 cccaggggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
 cccaggggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccagggtt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5					10					15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20					25					30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35					40					45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50					55					60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65					70					75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
				80					85					90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
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 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccaggg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgtttaatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

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Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
 1              5              10              15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
              20              25              30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
              35              40              45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
              50              55              60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
              65              70              75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
              80              85              90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
              95              100             105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
              110             115

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<210> 379

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
50 55 60

Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
65 70 75

Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
80 85 90

Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
95 100 105

Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
110 115 120

Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
125 130 135

Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
140 145 150

Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
155 160 165

Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
170 175

<210> 384
<211> 2379
<212> DNA
<213> Homo sapiens

<400> 384
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agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
atacagatgt ggcagctcag gtagccccc aaattgcctgga agaatacatc 150
atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
cccctcccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
tggtgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
atgttccaaa atcgggtccat ctcccaaggg gtccaatttt tcttcctggg 400
tgtcagcgag ccctgactca ctacagtga gctgacagg gctgtcatgc 450
aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
cactggttat agccccact gtottactga caatgctttc ttctgccgaa 600
cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650

ttgaactctg gtgactatca agggaacgog atgccccccc tccccttccc 2150
tctccctctc acttttggtg caagatcctt ccttggtcgt tttagtgcac 2200
tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
ttgtataaga ccctttactg attocattaa tgtcgcattt gttttaagat 2350
aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

				200					205					210
His	Leu	Glu	His	Asn 215	Gln	Phe	Ser	Lys	Leu 220	Asn	Leu	Ala	Leu	Phe 225
Pro	Arg	Leu	Val	Ser 230	Leu	Gln	Asn	Leu	Tyr 235	Leu	Gln	Trp	Asn	Lys 240
Ile	Ser	Val	Ile	Gly 245	Gln	Thr	Met	Ser	Trp 250	Thr	Trp	Ser	Ser	Leu 255
Gln	Arg	Leu	Asp	Leu 260	Ser	Gly	Asn	Glu	Ile 265	Glu	Ala	Phe	Ser	Gly 270
Pro	Ser	Val	Phe	Gln 275	Cys	Val	Pro	Asn	Leu 280	Gln	Arg	Leu	Asn	Leu 285
Asp	Ser	Asn	Lys	Leu 290	Thr	Phe	Ile	Gly	Gln 295	Glu	Ile	Leu	Asp	Ser 300
Trp	Ile	Ser	Leu	Asn 305	Asp	Ile	Ser	Leu	Ala 310	Gly	Asn	Ile	Trp	Glu 315
Cys	Ser	Arg	Asn	Ile 320	Cys	Ser	Leu	Val	Asn 325	Trp	Leu	Lys	Ser	Phe 330
Lys	Gly	Leu	Arg	Glu 335	Asn	Thr	Ile	Ile	Cys 340	Ala	Ser	Pro	Lys	Glu 345
Leu	Gln	Gly	Val	Asn 350	Val	Ile	Asp	Ala	Val 355	Lys	Asn	Tyr	Ser	Ile 360
Cys	Gly	Lys	Ser	Thr 365	Thr	Glu	Arg	Phe	Asp 370	Leu	Ala	Arg	Ala	Leu 375
Pro	Lys	Pro	Thr	Phe 380	Lys	Pro	Lys	Leu	Pro 385	Arg	Pro	Lys	His	Glu 390
Ser	Lys	Pro	Pro	Leu 395	Pro	Pro	Thr	Val	Gly 400	Ala	Thr	Glu	Pro	Gly 405
Pro	Glu	Thr	Asp	Ala 410	Asp	Ala	Glu	His	Ile 415	Ser	Phe	His	Lys	Ile 420
Ile	Ala	Gly	Ser	Val 425	Ala	Leu	Phe	Leu	Ser 430	Val	Leu	Val	Ile	Leu 435
Leu	Val	Ile	Tyr	Val 440	Ser	Trp	Lys	Arg	Tyr 445	Pro	Ala	Ser	Met	Lys 450
Gln	Leu	Gln	Gln	Arg 455	Ser	Leu	Met	Arg	Arg 460	His	Arg	Lys	Lys	Lys 465
Arg	Gln	Ser	Leu	Lys 470	Gln	Met	Thr	Pro	Ser 475	Thr	Gln	Glu	Phe	Tyr 480
Val	Asp	Tyr	Lys	Pro 485	Thr	Asn	Thr	Glu	Thr 490	Ser	Glu	Met	Leu	Leu 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
ggtccccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaatatg tcaagatoca gacttttcag tgtcacctca 100
gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tcctgctgct ggttttggtg 250
 gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300
 gagaccccgga attgattctc acaggcgcac catggcagtt tttgctgttg 350
 gagacttgga ctctatttat gggacagaag cagctgtgag tccaactggt 400
 ggaattcacc ttcaaactca aaccctgac ctatatcctg ttctgctcc 450
 atgttttggc cctttaggct cccacacctc atatgaagaa attgtaaaaa 500
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
 ggatgttgga aaaaattttg gtcatggaga tgtttaaata gtaaagtagc 700
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
 attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
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 tctgctttta actctttcct agcatgggtt ccataaaaaat tattataatt 900
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
 ccaacacggg gagaaaagaa aatttccctt ttacagtaa tgaatgtggc 1200
 ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr
 1 5 10 15

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
			20						25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
			80						85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
			95						100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
			110						115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
			125						130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
			140						145						

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 391
 cttttcagtg tcacctcagc gatctc 26

 <210> 392
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

 <400> 392
 ccaaaacatg gagcaggaac agg 23

 <210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
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accacaccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100
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<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

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His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
    35                      40                      45
Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
    50                      55                      60
Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
    65                      70                      75
Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
    80                      85                      90
Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
    95                      100                     105
Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
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Ser Gly Ser Ile Arg
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<210> 396
<211> 2639
<212> DNA
<213> Homo sapiens

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agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500
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ggcctgcctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 397
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 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
 95 100 105
 Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
 110 115 120
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
 125 130 135
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
 140 145 150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser
155 160 165

His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly
170 175 180

Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg
185 190 195

Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu
200 205 210

Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe
215 220 225

Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
230 235 240

Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
245 250 255

Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
260 265 270

Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
275 280 285

Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
290 295 300

His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
305 310 315

Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly
320 325 330

Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
335 340 345

Ala Ala Arg Gly Pro Thr Ile Leu
350

<210> 398
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 398
ccctgccagc cgagagcttc acc 23

<210> 399
<211> 23
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

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ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

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gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatattta 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgccac 750

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

 <400> 403
 ctctgtgggt ctccagattt caggccta 28

 <210> 404
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
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tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcgcat ttacagacac gtagtgtatt ctggaggctc aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccctttgg aaatcagtc tttggaggat gatggctggt gttattggcc 450
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<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
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1 5 10 15

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				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
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Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

315

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<400> 409
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cagcattttaa tgaaaaatth atgcttaaga agtaaaaatg gcaggcttcc 150
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Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu
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Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu
				95					100					105
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala
				110					115					120
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe
				125					130					135
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe
				140					145					150
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr							
				155										

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 411
 gtttgaggaa gctgggatac 20

 <210> 412
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 412
 ccaaactcga gcacctgttc 20

 <210> 413
 <211> 40
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

 <400> 413
 atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

 <210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
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aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtccctgtg aaaaacaatg 600
tgggcagagg octaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc cccgaagcca ttttagggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgctg ggaaggtgct 1100
gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
 <223> Synthetic construct.

<400> 416
 gccatagtca cgacatggat g 21

<210> 417
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 417
 ggatggccag agctgctg 18

<210> 418
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 418
 aaagtacaag tgtggcctca tcaagc 26

<210> 419
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 419
 tctgactcct aagtcaggca ggag 24

<210> 420
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 420
 atttctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgtcgc tctctctctc tctctctcac tctccctcc 200
ctctctctct gctgttcta gtctctagt cctcaaattc ccagtccct 250
gcaccccttc ctgggacact atgttgttct ccgccctcct gctggaggtg 300
atttgatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc 350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
cactggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
totgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa	cctaagagag	ctgctcccca	aacagctggg	gcagtacttc	900
cgctacaatg	gctcgctcac	aactccccct	tgctaccaga	gtgtgctctg	950
gacagttttt	tatagaaggt	cccagatttc	aatggaacag	ctggaaaagc	1000
ttcaggggac	attgttctcc	acagaagagg	agccctctaa	gcttctggta	1050
cagaactacc	gagcccttca	gcctctcaat	cagcgcattg	tctttgcttc	1100
tttcatccaa	gcaggatcct	cgtataccac	aggtgaaatg	ctgagtctag	1150
gtgtaggaat	cttggttggc	tgtctctgcc	ttctcctggc	tgtttatattc	1200
attgctagaa	agattcggaa	gaagaggctg	gaaaaccgaa	agagtgtggt	1250
cttcacctca	gcacaagcca	cgactgaggc	ataaattcct	tctcagatac	1300
catggatgtg	gatgacttcc	cttcatgcct	atcaggaagc	ctctaaaatg	1350
gggtgtagga	tctggccaga	aacactgtag	gagtagtaag	cagatgtcct	1400
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ggaagaactg	cagagccttc	agcctctcca	aacatgtagg	aggaaatgag	1500
gaaatcgctg	tggtgttaat	gcagaganca	aactctgttt	agttgcaggg	1550
gaagtttggg	atatacccca	aagtcctcta	ccccctcact	tttatggccc	1600
tttccctaga	tatactgcgg	gatctctcct	taggataaag	agttgctggt	1650
gaagttgtat	atttttgatc	aatatatattg	gaaattaaag	tttctgactt	1700
t	1701				

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<210> 423
<211> 337
<212> PRT
<213> Homo sapiens
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<400> 423
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
 1                    5                10                15
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
                20                25                30
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
                    35                40                45
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
                    50                55                60
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
                    65                70                75
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

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80										85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala					
				95					100					105					
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly					
				110					115					120					
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His					
				125					130					135					
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala					
				140					145					150					
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu					
				155					160					165					
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His					
				170					175					180					
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro					
				185					190					195					
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe					
				200					205					210					
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val					
				215					220					225					
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln					
				230					235					240					
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro					
				245					250					255					
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn					
				260					265					270					
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr					
				275					280					285					
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly					
				290					295					300					
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile					
				305					310					315					
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser					
				320					325					330					
Ala	Gln	Ala	Thr	Thr	Glu	Ala													
				335															

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 424
 gtaaagtcgc tggccagc 18

<210> 425
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 425
 cccgatctgc ctgctgta 18

<210> 426
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 426
 ctgcactgta tggccattat tgtg 24

<210> 427
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 427
 cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
 <211> 1073
 <212> DNA
 <213> Homo sapiens

<400> 428
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctccgga tcaggaaca 200
 ctacaaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300
 ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350
 gggttgaatg tacaacagca actgcacca catgtgttac caattttgt 400
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aaatcttcac gagcctcctc atccattcct tgttcccggg aggcacctg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaata 700
 agcaaataga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
 ctttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 429
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
 1 5 10 15
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
 20 25 30
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
 35 40 45
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
 50 55 60
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
 65 70 75

Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
80 85 90

Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr
95 100 105

Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro
110 115 120

Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly
125 130 135

Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp
140 145 150

Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln
155 160 165

Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp
170 175 180

Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His
185 190 195

Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln
200 205

<210> 430
<211> 1257
<212> DNA
<213> Homo Sapien

<400> 430
ggagagagggc gcgcgggtga aaggcgcatt gatgcagcct gcggcggcct 50
cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgccgc ctccccgcag cggctccgcg gctcctgct gctcctgctg 200
ctgcagctgc ccgcgccgc gagcgctct gagatcccca aggggaagca 250
aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
actacaagca gtgttcatgg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt taaaagatg cgttcaaata gtgctctaag 550
agttttgttc agtggctcac ttgcgctaaa atgcagaaat gcatgctgtc 600
agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttatTTT ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgcactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctotTTTT 900
ttattatgcc ttggaatggt tcacttaaat gacattttaa ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttaa atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
aatttgtaaa tgtaagaat tttttttata tctgttaaatt aaaaattatt 1250
tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1 5 10 15
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	
Leu	Pro	Lys													

<210> 432
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 432
 aggacttgcc ctcaggaa 18

<210> 433
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 cgcaggacag ttgtgaaaat a 21

<210> 434
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 435
cccacctgta ccaccatgt 19

<210> 436
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 436
actccaggca ccattctgttc tccc 24

<210> 437
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 437
aagggctggc attcaagtc 19

<210> 438
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 438
tgacctggca aaggaagaa 19

<210> 439
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
cagccaccct ccagtccaag g 21

<210> 440
<211> 19
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic oligonucleotide probe

<400> 440
gggtcgtgtt ttggagaga 19

<210> 441
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 441
ctggccctca gacaccaat 20

<210> 442
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 442
tcctccatca cttcccctag ctcca 25

<210> 443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
ctggcaggag ttaaagttcc aaga 24

<210> 444
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
aaaggacacc gggatgtg 18

<210> 445
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<400> 445
agcgtacact ctctccaggc aaccag 26

<210> 446
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 446
caattctgga tgaggtggta ga 22

<210> 447
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 447
caggactgag cgcttggtta 20

<210> 448
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 448
caaagcgcca agtaccggac c 21

<210> 449
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 449
ccagacctca gccaggaa 18

<210> 450
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 450
ccctagctga ccccttca 18


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<210> 451
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 451
tctgacaagc agttttctga atc 23

<210> 452
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 452
ctctccccct cccttttcct ttgttt 26

<210> 453
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 453
ctctggtgcc cacagtga 18

<210> 454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 454
ccatgcctgc tcagccaaga a 21

<210> 455
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 455
caggaaatct ggaaacctac agt 23

<210> 456
<211> 20
<212> DNA

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[illegible]

<223> Synthetic oligonucleotide probe

ccttgaaaag gaccagttt 20

<211> 22

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

atgagtcgca cctgctgttc cc 22

<211> 18

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

tagcagctgc ccttggtta 18

<211> 22

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